

## STIC Database Tracking Number: 9427

TO: Manjunath N Rao

Location: CM1/10D01/10A11

**Art Unit: 1652** 

Wednesday, May 28, 2003

Case Serial Number: 040863

10/040863

From: Susan Hanley

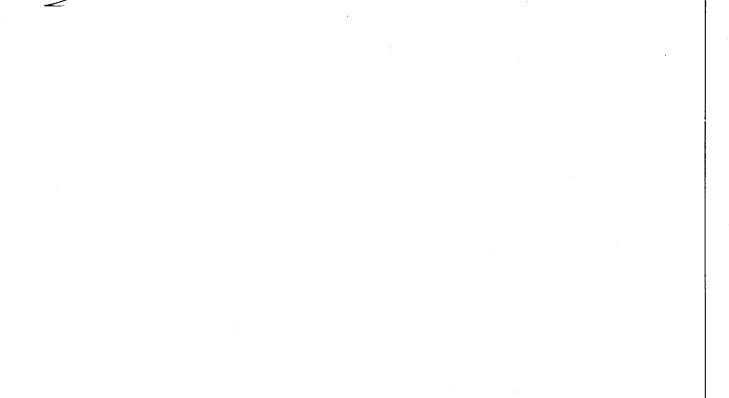
**Location: Biotech-Chem Library** 

CM1-6B05

Phone: 305-4053

susan.hanley@uspto.gov

## Search Notes





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Run on:

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Q9jk44 rattus norv
Q95087 rattus norv
Q91275 rattus norv
Q9j127 mus musculu
Q9002 mus spicile
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Q91460 mus musculu
Q920w3 mus musculu
Q91465 pan troglod
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Q9143 qorilla gor
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Q91450 homo sapien
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Q9jk44 rattus norv
                                                                         May 27, 2003, 15:01:52; Search time 37.5369 Seconds (without alignments) 1932.533 Million cell updates/sec
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                                                                                                                                                    1 LQQRIVKLQPLSEKELPMTT.....RSHFHLKAKGVTCYVAGRAF 353
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                                                                                                                                                                                                                                           671580
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                   671580 seqs, 206047115 residues
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Maximum Match 100%
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Q92OW2
Q91W60
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Q9TUD5
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sp_unclassified:*
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Maximum DB seq length: 2000000000
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|         | 9                           |           | 273  |       | O9TIC9                               |                      | O9ttc9 eulemur ful                |
| . 1     | 7 1                         | ė.        | 273  |       | Q9TTD0                               |                      | allit                             |
| . •     | 8                           | 4.        | 348  |       | Q9TUD1                               |                      | 09tudl macaca mula                |
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| 7       | 104                         | 5         | 365  |       | 014505                               |                      | 014505 homo sapien                |
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| •       | 5 104                       | 'n.       | 365  |       | 014506                               |                      | DIIIO.                            |
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| \       | 055025                      | PRELIA    | IINARY;  |       | PRT;                                 | 353 AA.              |                                   |
|         | 055025;                     | i         |  | (     | (                                    |                      |                                   |
|         | 01-00N-1998                 | (Treme    | SLrei.   | 000   |                                      | ence update)         |                                   |
|         | 01-MAR-2002                 | (Treme    | SLrel.   | 20,   | Last                                 |                      |                                   |
| DE      | Alpha 1,2 fucosyltransferas | ucosylt   | ransfe   | ras   | e (Fra                               |                      |                                   |
|         | Rattus norv                 | egicus    | (Rat)  |       | •                                    |                      |                                   |
|         | Eukaryota;<br>Mammalia: F   | Metazoa   | 1; Chordata<br>1. Podentia                     | dat   | a; Craniata; Ver<br>a: Sciurognathi: | tebrata;<br>Wuridae: | Eureleostomi;<br>Muripae: Raffus. |
| ) XO    | NCBI_TaxID=10116            | 10116;    |  | 4     | 3                                    |                      |                                   |
| RN      | [1]                         |           |  |       |                                      |                      |                                   |
| RP<br>0 | SEQUENCE FR                 | FROM N.A. | . (  |       |                                      |                      |                                   |
| 2 k     | STRAIN=BUFFALO RAT          | ALO KAL   | T.;  | 790-6 | 75030.                               |                      |                                   |
| A A     | Sherwood A                  | A I. HO.  | HOJMES F.H                                     | •     | ר<br>כ                               |                      |                                   |

Sherwood A.L., Holmes E.H.; "Cloning and expression of the catalytic domain from rat hepatoma H35 coll GDP-fucose: GMl alpha 1->2fucosyltransferase, an enzyme which is activated during early stages of chemical carcinogenesis in rat 

Arch. Biochem. Biophys. 355:215-221(1998). EMBL: AF042743; AAC14695.1; -. Interpro: PPR002516; GT 11. Pfam; PF01531; Glyco\_transf\_11; 1. liver.'

Result

353 AA; 39738 MW; 609D64EB222C9585 CRC64; Glycosyltransferase; Transferase. NON\_TER 1 1 SEQUENCE

Query Match

Gaps 0; 100.0%; Score 1896; DB 11; Length 353; 100.0%; Pred. No. 4.3e-164; ive 0; Mismatches 0; Indels 0; Best Local Similarity 100. Matches 353; Conservative

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1 LOGRIVKLOPLSEKELPMTTQMSSGNTESPENRRDSEQHGNGETRGMFTINSIGRLGNOM 60 g ά

GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120 

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GEYATLFALARMNGRLAFIPASMENALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
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                                                                  GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAMCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                 cell
                                                                                                                                                                                                                                                                                                                                                                                    Sherwood A.L., Stroud M.R., Levery S.B., Holmes E.H.;
An anino acid region at the N-terminus of rat hepatoma H35 cell
fucase:GMI alpha 1-2 fucosyltransferase is required for optimum octivity and interaction with lipids.";
Submitted (RMY-2000) to the EMBL, AF264005; AAF72200.1;
Interpro; IPR002516; GT_11.
Interpro; IPR002516; GT_11.
Glycosyltransferase; Transferase.
SEQUENCE 380 AA; 42742 MW; 920692C96689C05C CRC64;
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Pred. No. 4.7e-164;
0; Mismatches 0;
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100.0%;
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
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Best Local
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
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                                                                                                                                                                                                                                                                                                                                                                                    fucosyltransferase genes.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB006138; BAA21142.1;
Interpro; IPR002516; GT_11.
Pfam; PPC1531; GJyco_transf_11; 1.
GJyco_transf_11: 1.
GJyco_transferase, Transferase.
SEQUENCE 354 AA; 39995 MW; 8635444888215BAI CRC64;
                                                                                                                                                                                                                                                                                                                                           Soejima M., Wang B., Koda Y., Kimura H.;
"Two distinct rat GDP-L-fucose:b-D-galactoside 2-a-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha 1,2-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.1%; Score 1747; DB 11;
100.0%; Pred. No. 1.5e-150;
tive 0; Mismatches 0;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
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MEDLINE=21099374; PubMed=11179967;
PRT;
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PRELIMINARY;
                                                                                                                                                                       Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=COLON CANCER;
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Best Local Similarity
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                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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2.4.1.69).
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRHIPGHFVRFIGYPCSWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             Domino S.E., Zhang L., Lowe J.B.;
"Molecular Cloning, Genomic Mapping, and Expression of Two Secretor Molecular Cloning, Genomic Mapping, and Expression of Two Secretors Blood Group alpha (1,2) Fucosyltransferase Genes Differentially Regulated in Mouse Uterine Epithelium and Gastrointestinal Tract."; J. Biol. Chem. 276:23748-23756(2001).
BEBL; AF214656; AAR45146.1; -. MGD; MGI:109374; Put2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae: Mus.
NCBI_TaxID=10090;
Bureau V., Marionneau S., Cailleau-Thomas A., Le Moullac-Vaidye I Liehr I., Le Pendu J.;

"Comparison of the three rat GDP-L-fucose: beta-D-galactoside 2-alpha-L-fucosyltransferases FTA, FTB and FTC.";

Eur. J. Biochem. 288:1006-1019(2001).

EMBL; AF131238; AAD24469.1; -.

InterPro: IPR002516; GT_LI.

Pfam; PF01531; GJYCo_transf_LI; I.

GJYCOSYltransferase; Transferase.

SEQUENCE 354 AA; 39983 MW; 123E8C8379E8559E CRC64;
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89.0%; Pred. No. 1.4e-131;
ive 12; Mismatches 17; Indels 7;
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0
                                                                                                                                                                                                                                                                    Length 354;
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Pfam: PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
SEQUENCE 347 AA; 39243 MW; DD5F441046CC8E79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Alpha(1,2)fucosyltransferase FUT2 (EC 2.4.1.69).
                                                                                                                                                                                                                                                                    92.1%; Score 1747; DB 11;
100.0%; Pred. No. 1.5e-150;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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MEDLINE=21316545; PubMed=11323419;
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                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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SEQUENCE FROM N.A.
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Best Local Similarity
Matches 326; Conserv
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Q9JL27
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YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQARURGLKVNGSQPSTFV 180
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                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIXLANYTLPDSPF 300
                                                                                                           61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLVDWMBER 120
                                                                                                                                           261 LGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "GDP-fucose: beta-galactoside alphal, 2-fucosyltransferase, MFUT-II, and not MFUT-I or -III, is induced in a restricted region of the digestive tract of germ-free mice by host-microbe interactions and cycloheximide.";
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM
                                            DB 11; Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-202 (TrEMBLrel. 20, Last annotation update)
01-AMR-2002 (TrEMBLrel. 20, Last annotation update)
6DP-L-fucoses:beta-D-galactoside 2-alpha-1-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-ESTINAL TRACT;
STRAIN-ICR: TISSUE-CASTROINTESTINAL TRACT;
MEDLINE-20471982; Pubmed=11018479;
Lin B., Hayashi Y., Saito M., Sakakibara Y., Yanagisawa M., Iwamori M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.9%; Score 1534.5; DB 11; Lengt
88.7%; Pred. No. 3.1e-131;
Live 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
SEQUENCE 347 AA; 39215 MW; 616CCB11581C4179 CRC64;
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EMBL; AF064792; AAC16887.1; -.
MGD; MGI:109374; Fut2.
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247 LGDVVFAGNGIEGSPAKDFALLTQCNHTIXTIGFFGIWAAYLAGGDTIYLANYTLPDSPF 306
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                                                                                                                                                                                                                                                                                      STRAIN=VARIOUS STRAINS;
Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.;
"Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YRHIPGHEVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase (EC 2.4.1.69) (Fragment).
                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
(BDP-L-fucose:bbeta-D-galactoside 2-alpha-1-fucosyltransferase
(BC 2.4.1.69) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.2%; Score 1483.5; DB 11; Length 88.6%; Pred. No. 1.2e-126; ive 12; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB039115; BAB66638.1; --
EMBL, AB039116; BAB68639.1; --
EMBL, AB039116; BAB68640.1; --
EMBL, AB039117; BAB68641.1; --
EMBL, AB039119; BAB68643.1; --
EMBL, AB039119; BAB68643.1; --
EMBL, AB039119; BAB68643.1; --
EMBL, AB039120; BAB68644.1; --
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36516 MW; 0622D3BB503B72D1 CRC64;
    AA
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InterPro; PR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Iransferase.
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    PRELIMINARY;
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321 AA;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.; "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 LGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 306
                   201 GVHVRRGDYVHVMFKVWKGVVADRGYLEKALDRFRARYSSPVFVVTSNGMAWCRENINTS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSFVFVVTSNGMAWCRENINAS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 300
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GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 LGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIXLANYTLPDSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOORIVKLOPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM
                                                                               241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus spicilegus (Steppe mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.2%; Score 1483.5; DB 11; Length 321; 88.9%; Pred. No. 1.2e-126; Live 11; Mismatches 17; Indels 7;
                                                                                                                                                                                                                                                                                                                           0920W2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
2.4.1.69) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AB039123; BAB68647.1; ...
EMBL; AB039123; BAB68647.1; ...
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
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321 AA; 36560 MW; 5B7D19BA6D4B5394 CRC64;
                                                                                                                                                                                                                                                                                                              321
                                                                                                                                                                                       301 LKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 88.9
0; Conservative
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LKIFKPAAFLPEWM 321
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Gaps

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181 GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 VQQRLAKIQAM--WELPV------QIPVLASTSKALGPSQLRGWWTINAIGRLGNQM 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Evolution of alpha2-Fucosyltransferase genes in primates: relation between an intronic Alu-Y element and red cell expression of ABH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 HGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLDDSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 GVHVRRGDYVHVMPKVWKGVVADRRXLQQALDWFRARXSSPIFVVTSNGMAMCRENIDIS
                                                                                                                                                                                                                                 1 LOORIVKLOPLSEKELPMTTOMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNOM
                                                                                                                                                                                                                                                                         28 VQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGMWTINAIGRLGNQM
                                                                                                                                                                                                                                                                                                                    GEYATLFALARMNGRLAFIPASMHNALAPIFRISEPVLHSDTAKKIPWONYHLNDWMEER
                                                                                                                                                                                                                                                                                                                                                                                                  121 YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Pan.
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                                                                                                                                                 DB 6; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apoil P.-A., Roubinet F., Despiau S., Mollicone R., Oriol
                                                                                                                                                                                        Indels
J. Biol. Chem. 270:4640-4649(1995).

EMBL; AB015635: BAA31128.1; -
InterPro; IPR002516; GT_11.

Pfam; PF01531; Glyco_transf_11; 1.

Glycosyltransferase.

SEQUENCE 343 AA; 38973 MW; 894E28BD74AEBFBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 AA; 38428 MW; E7FABAOFF1BC95F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.9%; Score 1400.5; DB 6; 79.8%; Pred. No. 4.8e-119; Live 25; Mismatches 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 LKVFKPEAAFLPEWVGIPADLSPLLK 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Biol. Evol. 17:337-351(2000).
EMBL, AF080604; AAF14066.1; -
InterPro: IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
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MEDLINE=20188794; PubMed=10723735;
                                                                                                                                           Query Match
Best Local Similarity 79.8'
Matches 260; Conservative
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Best Local Simi
Matches 259;
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Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.;
"The old origin of a null allele se428 of the human ABO-secretor type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 YRHIPGHFVRFIGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
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MEDILINE=9181460; Pubmed=7876235;
Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;
"Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucosyltansferase gene (FUT2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                                                                                                                     STRAIN=NJL/MSF;
Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.;
"Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 LQQQIVKLQTLSEKEL-QAVQMSSPNAARTDMQQ-----SAKLQGIFTINSIGRLGNQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 LGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
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                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotā; Metazoā; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                  Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB039122; BAB68646.1;
InterPro: IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                       321 AA; 36464 MW; FF5304CD150F774A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha(1,2) fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                77.5%; Score 1468.5; DB 1
87.9%; Pred. No. 2.8e-125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 87.99
Matches 277; Conservative
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307 LKIFKPAAAFLPEWM 321
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                                                                                                                                                                                                                                                                                                                                   321
musculus (Mouse).
                                                                                                      SEQUENCE FROM N.A.
                                                            NCBI_TaxID=10090;
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                                                            180
                                                                                                                          240
                                                                                                                                                                                      300
                 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95181466; PubMed=7876235;
Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;
"Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucosyltansferase gene (FUT2).";
J. Biol. Chem. 270:4640-4649(1995).
EMBL: AB015634: BAA31127.1:
Interpro: IPR002516: GT_11.
Fign: PF01531: Glyco_transf_11; 1.
Glycosyltransferase: Transf_erase.
SEQUENCE 343 AA; 38999 MW; B849D7E152852081 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 VQORLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGMWTINAIGRLGNQM 76
                                                                         GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER
                                                          121 YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
                                                                                                                      181 GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                          241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                            AA.
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                                                                                                                                                                                                                                                                                                                                                                                         Created)
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01-NOV-1998 (TEBMBLrel. 08, Cre
01-NOV-1998 (TEBMBLrel. 08, Las
01-MAR-2002 (TEBMBLrel. 20, Las
Alpha(1,2)fucosyltransferase.
FUT2.
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nes 259; Conservative
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257 HGDVVPAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYILFDSPF 316
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Blancher A.,
Brancher A.,
Broulution of alpha2-Fucosyltransferase genes in primates: relation between an introduc Alu Y element and red cell expression of ABH antigens."

Mol. Biol. Evol. 17:337-351(2000).

EMBL; AF080606; AAF14068.1; -
InterPro: IPR002516; GT_11.

Fransferase.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343 AA; 39001 MW; A753375D47AE8C8C CRC64;
                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
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(TrEmBLrel. 13, Last seq
(TrEmBLrel. 20, Last ann
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02, Last seq
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MEDLINE=20188794; PubMed=10723735;
                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Crea 01-MAY-2000 (TrEMBLrel. 13, Last 001-MAR-2002 (TrEMBLrel. 20, Last Alpha (1,2) fucosyl transferase.
                                                                                                                                                                                                                                                                                                                                                       Gorilla gorilla (gorilla)
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                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9593;
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Q29505;
Q1-FEB-1997 (
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Best Local Simi
Matches 259;
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Hitoshi S., Kojima N., Tadazawa I., Tsuji S.;

Hitoshi S., Kojima N., Tadazawa I., Tsuji S.;

Micose: beta-D-galactoside 2-alpha-L-fucosyltransferase.*;

Tucose: beta-D-galactoside 2-alpha-L-fucosyltransferase.*;

J. Biol. Chem. 271:16975-16981(1996).

-! FUNCTION: CREATES A MEMBRANE-ASSOCIATED PRECURSOR OLIGOSACCHARIDE

FUC-ALPHA(1,2)GALBETA-) CALLED THE HANTIGEN WHICH IS AN

ESSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE MEMBRANE-ASSOCIATED

A AND B ANTIGEN SYNTHESIS PATHWAY. HAND SE ENZYMES FUCOSYLATE THE

SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.

-!- CATALYTIC ACTIVITY: GDP-L-FUCOSYL-R = GDP -

ALPHA-L-FUCOSYL-1, 2-BETA-D-GALACTOSXL-R = GDP -

--- PATHWAY: GLYCOSYLATION.

-!- PATHWAY: GLYCOSYLATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND

C-!- PATHWAY: GLYCOSYLATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND

C-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND

C-!- STREED SPECIFITY: ADULT GASTRONTESSTINAL FRACT AND COLON.

-!- STREED SPECIFITY: ADULT GASTRONTESSTINAL FRACT AND FUT3) WHICH

ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE IN RABBIT. THEY ARE

C-!- STREED IN A TISSUE-SPECIFIC MANNER.

-!- STRILANTIY: STRUCTURAL SIMILARITY WITH THE OTHER MAMMALIAN

C-!- STRUCTURAL SIMILARITY WITH THE OTHER MAMMALIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
U1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Galactoside 2-L-fucosyltransferase 3 (EC 2.4.1.69) (Secretor blood
group ALPHA-2-fucosyltransferase) (GDP-L-fucose:beta-D-galactoside
2-ALPHA-L-fucosyltransferase) (ALPHA(1,2)FT) (Fucosyltransferase 3
orycologus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelecstomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
746F7007309862A5 CRC64;
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InterPro; IPR005516; GT 11.
Pfam; PF01531; Glycosyltransf-11; 1.
Iransferase, Glycosyltransferase; Glycoprotein; Iransmembrane; Signal-anchor; Golgi stack.
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SEQUENCE FROM N.A.
TISSUE-GASTROINTESTINAL TRACT,
MEDLINE-96279281; PubMed-8663168;
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192
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386
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347 AA;
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Gaps
                                                 7;
    73.4%; Score 1391.5; DB 6; Length 347; 79.8%; Pred. No. 3.2e-118; tive 25; Mismatches 34; Indels 7;
Query Match
Best Local Similarity 79.8:
Matches 260; Conservative
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LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60

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GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                            YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 180
 LOCRLVRIOPTWEELLPAL-----TPAVTFRPTSORAPSRPLGGMWTINAMGRLGNOM 80
 28
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GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 201 241

LKVFKPEAAFLPEWVGIPADLSPLLK 326 301 ò g

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SEQUENCE FROM N.A.

KGOA Y., Tachida H., Soejima M., Takenaka O., Kimura H.;

"The old origin of a null allele se428 of the human ABO-secretor type alpha(1,2) fucosyltransferase gene (FUT2).";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-95181460; PubMed=7876235;
Kelly R.J., Roqquier S., Glorgi D., Lennon G.G., Lowe J.B.;
Kelly R.J., Roqquier S., Glorgi D., Lennon G.G., Lowe J.B.;
Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucosyltansferase gene (FUT2).";
J. Biol. Chem. 270:4640-4649(1995).
EMBL; ABO15635; BAAA1129.1;
InterPro; IPR002516; GT_ll.
Pfam; PF01531; Glyco_transf_ll; 1.
Glycosyltransferase; Transferase.
SEQUENCE 343 AA; 38973 MW; 2BD4D2A9704F4A0C CRC64;
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                                                                                                                                                         Pongo
                                                                                                                                                                                                                                                                                                                                                                                                                                      73.3%; Score 1389.5; DB 6; Leust...
70.1%; Pred. No. 4.8e-118;
70.1%; Pred. no. 4.8e-118;
                                                                                                                                         Craniata; Vertebrata; E
Catarrhini; Hominidae;
                                                                     Last sequence update)
Last annotation update)
                             343 AA
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                             PRT;
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Mammalia; Eutheria; Primates;
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                                                                   (TrEMBLrel. 08, (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 79.1%;
                                                        (TrEMBLrel. 08,
                                                                                                                             Pongo pygmaeus (Orangutan)
                             PRELIMINARY;
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                                                                                                                                                                     NCBI_TaxID=9600;
                                                      01-NOV-1998 (
01-NOV-1998 (
01-MAR-2002 (
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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                                    OM nucleic - nucleic search, using sw model
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Perfect score:
                                                                                                                                Scoring table:
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                                                                                                              Sequence:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |             | сЮ    |             |      |             |                |
|---------------|-------------|-------|-------------|------|-------------|----------------|
| Result<br>No. | 9 1         | uery  | ، ب         | DB   | qi          | ription        |
| ;-1 C         | 1149        | 100.0 |             | 10   | AF264005    | F264005 Rattus |
| a W           | <br>n       | <br>  | 86          |      | 138         | 0138 Rattu     |
| 4             | 121.        | 7     | 8           |      | 111         | 211 Rattus n   |
| 5             | 106         | m     | 90          | 10   | 7           | 12743 Rattus   |
|               | H           |       | 676         | 10   | 9           | 14656 Mus mus  |
| ر<br>ان       | 3.          | ·<br> | 77          | 7    | 40          | 3/74 Mus m     |
| 000           | 0<br>0<br>0 | n c   | 40          | TC   | 3\ r        | 04/92 Mus mus  |
| y C           | > c         | n a   | ρц          | ) C  | 7 5         | 39114 MUS      |
| 9 -           |             | `σ    | ) VC        | 9 0  | 1 -         | 19116 Mus mus  |
| 12            | 0           |       | v c         | 10   | 111         | 89117 Mus mas  |
| 13            | 0           | 6     | 9           | 10   | 11          | 39118 Mus mus  |
| 14            | 0           | 9     | Θ           | 10   | 111         | 39119 Mus mus  |
| 15            | 0           | σ,    | w           | 10   | 312         | 39120 Mus mus  |
| 16            | 0           | 9.    | S           | 0    | 112         | 19123 Mus spi  |
| 17            | 00          | σ,    | Θ           | 10   | 312         | 39121 Mu       |
| 18            |             | σ.    | 96          | 10   | 112         | 39122 Mus mu   |
| 19            | 69.         | ω.    | 55          | 10   | 23          | 31239 Rattus   |
| 20            | 59.         | 7     | 10          | 10   | 21          | 39213 Mus spi  |
| 21            | 65          | ۲.    | 70          | 10   | 320         | 89209 Mus mu   |
| 22            | 54.         | 7     | 10          | 10   | 321         | 39212 Mus mus  |
| 23            | 54          |       | 10          | 10   | 223         | 13532 Mus      |
| 24            | 54.         | ٠,    | 28          | 10   | - I         | 382 M.muscula  |
| 72            | 53.         | ٠,    | 07          | 07   | 920         | 39206 Mus      |
| 7.0           |             | ه ر   | 10          | 0 7  | 920         | 39207 Mus mus  |
| 7 0           | 55.         | ٠,    | 70          | 70   | 320         | 39208 Mus      |
| 200           |             | o v   | $\supset c$ | 7 -  |             | SULL MUS MUS   |
| 10            | , r         | > u   | > 1         | 7 -  | 2 5         | L#OJ/ Mus mus  |
| 0 5           | . TO        | 0 u   | 7 6         | 7 -  | 7 0         | SOLO MUS MUS   |
| 7 (           | n t         | ٠,    | 7.0         | T C  | 076         | 59204 Mus      |
| 75            | ç<br>Ç      | Ġ     | 7.0         | 0 .  | 226         | SUM SOM COZAS  |
| 55            | . (4)       | ٠,    | 7 :         | ₫.   | 7           | oy O. cumicul  |
| 4, 0          | ,           | n L   | 40          | 4 -  | $\tilde{y}$ | odys sus scro  |
| 200           |             | n 1   | 7 .         | 4.   | 0 0         | SI SUS SCIOLA  |
| 9 6           |             | ი.    | 04          | 4 ,  | 2           | 304 Sus scr    |
| 7 0           |             | 4.    | 200         | ه د  | 2 5         | 263            |
| 9 0           | 900         | * •   | 70          | 0 (  | 7           | 1027 Sequence  |
| n -           | , K         |       | 0.4         | ρ,   | 7 0         | TOT Sednence   |
| 4.            |             | . 4   | 35          | 2,   | 9           | 14658 Mus mus  |
| 4.            | 17          | 'n.   | 90          | י עכ | 2           | 0035 60        |
| 4.2           | 9           | 'n    | 106         | n    | ŏ           | Jene Gorilla   |
| 43            | ٠           | m     | 63          | σ,   |             | 3888 Homo sap  |
| 44            | 13.         | m,    | 78          | o 1  | 5           | 1899 Homo sap  |
| 45            | 2           | ~     | Z           | ĸ    | 7           | 3079 Sequence  |

Rattus norvegicus alpha 1-2 fucosyltransferase mRNA, complete cds. AF264005 AF264005 Rattus.
1 (bases 1 to 1149)
Sherwood,A.L., Stroud,M.R., Levery,S.B. and Holmes,E.H.
An amino acid region at the N-terminus of rat hepatoma alphal-->2 Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; ALIGNMENTS Rattus norvegicus. ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AF264005 LOCUS DEFINITION REFERENCE AUTHORS TITLE

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009 009 099 99 720 720 780 780 840 840 900 006 960

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961 ACCCTTCCGGATTCTCCGTTCCTCAAGTCTTTAAGCCAGGCAGCCTTCCTACCCGAA 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bureau, V., Marionneau, S., Cailleau-Thomas, A., Le Moullac-Vaidye, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                 901 ACCTTTGGGATTTGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTAC
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     541 CTGCATGACCACGTGCGGGAGGAGGCCCAGGCCTTCCTGCGTGTCTGCGGGTGAATGGG
                               CCTAATGTGTGGAAGGGCGTGGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATG
                                                                                                                                                                                                                                                     661 CCTAATGTGTGGAAGGGCGTGGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATG
                                                                                                                                                                                                                                                                                                                                                                                                     781 CGGGAGAACATTAATGCTTCCCGAGGAGACGTGGTGTTCGCGGGCAATGGTATTGAGGGG
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1847 bp DNA linear 'ROD 08-1,2-fucosyltransferase B (FTB) gene,
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Comparison of the three rat GDP-L-fucose:beta-D-galactoside
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2-alpha-L-fucosyltransferases FTA, FTB and
Eur. J. Blochem. 268 (4), 1006-1019 (2001)<sup>2</sup> 21099374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Rattus norvegicus alpha 1
complete cds.
AF131238 AF131238.1 GI:4580572
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Rattus norvegicus
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fucosyltransferase modulates enzyme activity and interaction with lipids: strong preference for glycosphingolipids containing terminal Galbetal-->SGAINAC-structures Biochemistry 40 (19), 5708-5719 (2001)
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                                                                                                                                                                                                                           , Northwest
USA
                                                                                                                                             2 (bases 1 to 1149)
Sherwood, A.L. and Holmes, E.H.
Direct Submission
Submitted (05-MAY-2000) Molecular Medicine,
                                                                                                                                                                                                                                                   Seattle, WA 98134,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="glycosyltransferase'
                                                                                                                                                                                                                                                                                                                                      /strain="Fischer"
/db_xref="taxon:10116"
/cell_line="Reuber H35 h.
                                                                                                                                                                                                                                                                     Location/Qualifiers
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   ASCCAGCCGAGTACTTTGTGGGTGTCCATGTGCGCCGAGGGGGACTATGTGCATGTCATG 870
                                   CCTAATGTGTGGAAGGGCGTGGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATG 720
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Submitted (04-AUG-1997) Yoshiro Koda, Kurume University, School
Medicine, Department of Forensic Medicine, Asahimachi 67, Kurume
Fukucka 830, Japan (E-mail:ykoda@med.kurume-u.ac.jp,
Tel:0942-31-7554, Fax:0942-31-7700)
                                                         CCTAATGTGGAAGGGCGTGGCTGGCTGACCGGGGTTACCTGGAAAGGCCCTGGATATG
                                                                                                                                                                                  TTCCGGGCACGCTAITCATCTCCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGC
                                                                                                                   CGGGAGAACATTAATGCTTCCCGAGGAGACGTGGTGTTCGCGGGCAATGGTATTGAGGGG
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AB006138 AB006138 GI:2317265
FTB; alpha 1,2-fucosyltransferase.
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Rattus norvegicus
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Two distinct rat GDP-L-fucose:b-D-galactoside
2-a-L-fucosyltransferase genes
Unpublished
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*protein_id="AAD24469.1"

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LAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFYRFTG
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VMPNVWRGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGN
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AAFLPEWVGIPADLSPLLKH"
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                                                                                                                                                                                             /note="glycosyltransferase; alpha 2-fucosyltransferase
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                                                                                                                                             Product="alpha 1,2-fucosyltransferase
organism="Rattus norvegicus"
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<211. .>127
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/product=*alpha 1,2-fucosyltransferase"
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S worley, K.C.

Direct Submission

Direct Submission

Submitted (16 MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 150840)

Worley, K.C.

Direct Submission

L. Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 19, 2002 this Sequence version replaced gi:20806241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is
Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Socht, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Sutton, A., Tavek, A., Tabor, P., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Verra, V., Villalon, D., Vinson, R., Wang, S., Wand-Moore, S., Warren, R., Washington, C., Watlington, S., Wulliamson, A., Wleczyk, R., Wooden, S., Weistock, G., Wulliamson, A., Wleczyk, R., Wooden, S., Weistock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 106837 bases at least 030
Consensus quality: 113151 bases at least 030
Consensus quality: 115417 bases at least 020
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Rattus norvegicus alpha 1,2 fucosyltransferase mRNA, partial cds. AF042743.
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SSPVFVYTSNGMAMCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFG
IWAAYLAGGDTIYLANYTLPDSPFLKVFKPERAAFLPEWVGIPADLSPLLKALTPACPR
GTCGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCACCATCATGACTATTGG 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sherwood, A.L. and Holmes, E.H. Cloning and expression of the catalytic domain from rat hepatoma H35 cell GDP-fucose: GML alpha 1-->2fucosyltransferase, an enzyme which is activated during early stages of chemical carcinogenesis
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25, USA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleost
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Submitted (13-JAN-1998) Cell Surface Biochem., Nor'
120 Northgate Plaza, Suite 230, Seattle, WA 98125,
Location/Qualifiers
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/db_xref="taxon:10116"
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MHNALAPIFRISLPVLHSDTARRIPWQNYHLNDWMEBRYRHIPGQYVRFTGYPCSWTF
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                                                                        linear ROD 26-JUN-2001
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                                                                                                                                                                                  Bukaryota. Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 6762)
Domino, S.E., Zang, L. and Lowe, J.B. on dexpression of two secretor blood group alpha (1,2)fucosyltransferase genes differentially regulated in mouse uterine epithelium and gastrointestinal tract J. Biol. Chem. 276 (26), 23748-23756 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="fucosyltransferase; similar to the Mus musculus strain ICR Sec2 sequence deposited at GenBank Accession Number AF064792; similar to the Homo sapiens secretor blood group alpha(1,2)fucosyltransferase FUT2 sequences deposited at GenBank Accession Numbers D87942 and U17894/codon_start=1
                                                                                                                                                                                                                                                                                                                                           7 (bases 1 to 6762)
Domino,S.E. and Lowe,J.B.
Mus musculus alpha(1,2)fucosyltransferase FUT2 (Sec2) genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Michigan, 1150 W. -0650, USA
                                                                          6762 bp DNA linear ROD 26-
alpha(1,2)fucosyltransferase FUT2 (Fut2) gene,
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   1021 GCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTCTGATGGGAA 1068
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2210. .3253
/gene="Fut2"
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/protein_id="AAF45146.1"
/db_xref="GI:7288505"
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/cell_line="E14"
/cell_type="E5"
<2210. .>3253
/gene="Fut2"
/note="Sec2"
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3 (bases 1 to 6762)
Domino, S.E. and Lowe, J.B.
Direct Submission
Submitted (13-DEC-1999) HHMI, Universi
Ctr. Dr., Ann Arbor, MI 48109-0650, US
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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/gene="Fut2"
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               Mismatches
             0;
100.0%;
             Matches 1068; Conservative
Best Local Similarity
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| Db 3209 TGGATGGGCATCCCGGAGACCIGTCCCCACTTAAGCACTAACAACCAGCTGTCT 3268  QY 1081 CGGTCCCACTTCCACCTCAAGGCAAAAGGAGTCACTTGTTAGGTCGCAGGAAGAGCTTC 1140  LIIII   | p DNA linear HTG 18-JUL. WORKING DRAFT SEQUENCE, 14 order  | Mammalia: Butheria; Rodentia; Sciurognathi; Muridae; Mus.  REFERENCE 1 (bases 1 to 200146)  AUTHORS DOE Joint Genome Institute.  TITLE Sequencing of Mouse JOURNAL Unpublished  REFERENCE 2 (bases 1 to 200146)  AUTHORS DOE Joint Genome Institute.  TITLE Direct Submission   | JOURNAL Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA COMMENT On Jul 18, 2000 this sequence version replaced gi:8810391. Genome Center Center Center Center Joint Genome Institute Center Code: JGI Web site: http://www.jgi.doe.gov | Project Information Center Project Name: 1750833 Center clone name: RPCI-23_36F17 Summary Statistics Consensus quality: 191947 bases at least Q40 Consensus quality: 197212 bases at least Q30 |   | of the gaps between them are based on estimates that provided by the submittor.  This sequence will be replaced by the finished sequence as soon as it is available a the accession number will be preserved.  1 16256 contig of 16256 bp in length 16357 16356; gap of unknown length 16357 38024; contig of 21668 bp in length  | * 38025 38124: gap of unknown length<br>* 60460 6059; contig of 22335 bp in length<br>* 60460 6059; gap of unknown length<br>* 60560 66982: contig of 6423 bp in length<br>* 66983 67082; captig of 6423 bp in length<br>* 106954 107053: gap of unknown length<br>* 107054 111366: contig of 4313 bp in length<br>* 111467 113014: contig of unknown length<br>* 111467 113014: contig of unknown length<br>* 113015 113114: gap of unknown length |
|--|--|---|---|--|---|---|---|
| Best Local Similarity   89.7%;   Pred. No. 1.3e-238;   Radels   21;   Gaps   2;   Aatches 1031;   Conservative   0;   Mismatches   97;   Indels   21;   Gaps   2;   2210   AIGGCAGCGCCCAGTCCTTCCTTTCTTCTTTGTCTTC   0 | QY         121 AAGGAATTACCGATGACGACTCAAATGTCCTCGGGAAACACAGAAGCCCAGAGATGCGA 180           Db         2330 AAGGAATTACAGGCGTTCAAATGTCCTCACCAACGCGGCAAGAACAGACAT 2382           QY         181 CGGACAGCAGCAGCATGGGAATGGAGATCCACCAACGGGCATCAATTCACGATCAATTCCATT         240           Db         2383GCAGCAGGGAATGGAGATGCAGGCATATTCACGATCAATTCCATC         2428           QY         241 GGCCGGGAACCAGATGGCGAATACGCCACACTTTGCACTGGCAGATGAAT         300           CA         111111111111111111111111111111111111 | 301 GGACGCTTGCGTTCATCCCCGCATCCATGCACCTCTAGCGCCCATCTTCAGGATC 301 GGACGCTTGCGTTCATCCCCGCATCCATGCACACCTCTAGCGCCCATCTTCAGGATC 2489 GGTCGCGTTTACACACGACAAAAAAACATCCATGCAGAATTACCATCTC 361 AGCCTCCCGGTGTTACACACGACAAAAAAAACATCCCATGCAAAATTACCATCTC 2549 AGCTCCCCGGTGTTACACAACAACAACAAAAAAACATCCCATGCAAAATTACCATCTC 2549 AGCTCTCCCGGTGTTACAAAAAAAAAAAAAAAAAAAAAA | 421 AACGACTGGAGGGGGGTTACCGCCACATTCCGGGACACTTTGTGCGCTTCACGGGA  1111111111111111111111111111111   | 541 CTGCATGACCACGTGCGGAGGAGGCCCTCCTGCGTGGGTCTGCGGGTGAATGGG 11111 1111 11111 11111 11111 11111111   | Db         2789 AGCCAGCCGAGTACCTTGTGGGGGGCTCATGTGCATGTGCATG         2848           Qy         661 CCTAATGTGGAGGGGGTGGCTGCCGGGGTTACCTGGAAAGGCCCTGGATATG         720           I         11   111111111111111111111111111111111 | QY         781 CGGGAGAACATTAATGCTTCCCGAGGAGCGTGGTGTTCGCGGGCAATGGTATTGAGGGG 840           DD         2969 CGGAGAACATCAACACCTCCCTAGGAGACGTGTTTGCGGGCAATGGTATTGAGGC 3028           QY         841 TCGCCAGCCAAGGACTTCGCGCTGCTGCACCACCACCATCATTGG 900           DD         3029 TCACCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCATCATTGG 900           DD         3029 TCACCAGCCAAGGACTTCGCGCTCCTCACCCAGTGCAACCACCATCATGGA 3088 | OY 901 ACCTTTGGGATTTGGGCTGCCTACCTGGCAGGTGGTACCATCTACTTAGCCAACTAC 960  |

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Biochim. Biophys. Acta 1487 (2-3), 275-285 (2000)
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1044)

Lin, B., Hayashi, Y., Saito, M., Sakakibara, Y., Yanagisawa, M. and

Iwamori, M.
                                         841 TCGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCATCATGACTATTGGG
                         TTCCGGGCACGCTATTCATCTCCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGC
                                                                                                                                                                                                                                901 ACCTTTGGGATTTGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTAC
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Lin,B., Hayashi,Y., Saito,M., Sakakihara,Y., Yanagisawa,M.
Iwamori,M.
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Submitted (12-MAY-1998) Chemistry, Faculty of Selence & 7
Kinki University, Kowakae, Higashi-osaka 577-8502, Japan
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Mus musculus GDP-L-fucose:beta-D-galactoside
2-alpha-1-fucosyltransferase mRNA, complete cds.
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/db_xref="taxon:10090"
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1: contig of 4877 bp in length
1: gap of unknown length
2: contig of 28326 bp in length
3: contig of 8071 bp in length
3: gap of unknown length
4: gap of unknown length
5: gap of unknown length
7: contig of 1835 bp in length
7: contig of 1835 bp in length
7: gap of unknown length
7: gap of unknown length
8: contig of 38205 bp in length
9: contig of 3164 bp in length
9: contig of 3164 bp in length
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52711 c 50595 g 48057 t 1301 others
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                                                                                                                                                                                                                                                                                                                                                                                 81.1%; Score 931.8; DB 2;
89.7%; Pred. No. 1.5e-238;
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                         /organism="Mus musculus"
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                                                                                                                                                                                                                            Location/Qualifiers
1. .200146
                                                   146517:
154588:
154688:
158642:
158742:
160577:
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Matches 1031; Conservative
1113115
1117992
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us-10-040-863-7.rge

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Mus misculus FUT2 gene for GPP-L-fucose.beta-D-galactoside
2-alpha-1-fucosyltransferase, partial cds, strain:G57BL/10snJ.
AB039114
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2-alpha-1-fucosyltransferase"
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                                                                                                                                ACCCTTCCGGATTCTCCGTTCCTCAAAGTCTTTAAGCCAGAGGCAGCCTTCCTACCCGAA 1020
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RFRARYSSPVFVVTSNGMAWCRENINTSLGDVVFAGNGIEGSPAKDFALLTQCNHTIM
                                                                                                                                                                                                                                                                                                                                                                                                 FUT2; GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase.
Mus musculus (sub_species:domesticus, strain:C57BL/10SnJ) DNA.
Mus musculus
                 Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of Five Mus musculus subspecies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. (bases 1 to 963)
Liu, Y. and Saitou, N.
Direct Submission
Submitted (29-FEB-2000) Naruya Saitou, National Institute of
Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Mishima,
Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp,
URL:http://sayor.lab.nig.ac.jp/, Tel:81-559-81-6790,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                TCGCCAGCCAAGGACITCGCGCTGCTCACCCAGTGCAACCACCATCATGACTATIGGG
                                                                ACCTITGGGATTIGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu,Y., Kitano,T., Koide,T., Shiroishi,T., Moriwaki,K. Saitou,N. Conspicuous Differences among Gene Genealogies of 21 Nu
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia;
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KEYWORDS
SOURCE
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 /procein_id="MAGACI6887.1"
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KGFALLTQCCHTIMITGTFGIWAAYLAGGDTIYLANYTLPDSSPELKIFKPAAAFLDEW
MGTRADLSGPLLKH

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Pred. No. 6.1e-221;
0; Mismatches 82;
                                                                                                                                                                                                     Match 75.4%;
Local Similarity 90.3%;
ies 956; Conservative
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Length 963;

DB 10;

802;

Score

69.8%;

Query Match

ABU39115 963 bp DNA linear ROD 02-OCT-2001 Mus musculus FUT2 gene for GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase, partial cds, strain:BFM/2Msf. ABG39115 /product="GDP-L-fucose:beta-D-galactoside
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/db\_xref="GI: AB039115.1 GI:15822975 FUI2: GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase. ä Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of Five Mus musculus subspecies
Unpublished 2 (bases 1 to 963)
Liu, Y. and Saitou, N.
Direct Submission
Submitted (29-FBB-2000) Naruya Saitou, National Institute of
Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Mishima,
Shizuoka 411-8540, Japan (P-mail:nsaitou@genes.nig.ac.jp,
UKL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790, 3 ITCCTCATCTTTGTCTTCGTGACTTCCACCATCATCACCTCCAGCGGAGTAGTGAAG 102 3 CTCCAACCCCTGTCAGAGAAGGAATTACCGATGACGACTCAAATGTCCTCGGGAAACACA 162 GAAAGCCCAGAGATGCGACGGGACAGCGAGCAGCATGGGAATGGAGAGCTGCGGGGCATG 222 TTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACACTCTTT 282 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 TICCICATOTITGICITITGIGACTICCACCATCATCACCACCACCAGCAACGAATAGIGAAG Mus musculus (sub\_species:brevirostris, strain:BFM/2Msf) DNA. Mus musculus 21; Gaps Liu,Y., Kitano,T., Koide,T., Shiroishi,T., Moriwaki,K. and Saitou,N. Ö /note="sequence used for primer design based Acc#AF064792" Score 802; DB 10; Length 963; Pred. No. 7.6e-204; 0; Mismatches 75; Indels 2: /strain="BFM/2Msf" /sub\_species="brevirostris" /db\_xref="taxon:10090" /chromosome="7" /organism="Mus musculus" /EC\_number="2.4.1.69" /note="Sec2; Se" Location/Qualifiers /codon\_start=1 69.8%; 90.2%; /gene="FUT2" <ī. .>963 /gene="FUT2" 188; Conservative Similarity m Dp ð

ΩŸ Dp á g δy qq  $^{\circ}$ qq δy g

qq QΥ OD

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/product="GDP-L-fucose:beta-D-galactoside
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285 c 257 g 207 t
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Liu,Y. and Saitou,N.
Direct Submission
Submitted (Marsian)
Submitted (Marsian)
Submitted (Marsian)
Submitted (Marsian)
Submitted (Marsian)
Genetics, Laboratory of Evolutionary Genetics; 1111 Yata,
Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp,
URL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790,
Fax:81-559-81-6789)
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Pred. No. 7.6e-204;
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                                                                                                                                            1. .963
/organism="Mus musculus"
                                                                                                                                                                              /strain="BLG2/Msf"
/sub_species="musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                             /EC_number="2.4.1.69"
/note="Sec2; Se"
                                                                                                                           Location/Qualifiers
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/gene="FUT2"
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                           280 GCGCCCATCTCAGGATCAGTCTCCCGGTGTTACACAGCGACACCAGCAGAAGGATCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCAGAATTACCATCTCAACGACTGGATGGAGGAGCGTTACCGCCACATTCCGGGACAC
                                                                                                                                                                                  643 GACTATGTGCATGTCATGCCTAATGTGTGGAAGGGCGTGGTGGCTGACCGGGGTTACCTG
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                GCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGGGGCACAGGGCCAAAAAGATCCCA
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Mus musculus (sub_species:castaneus, strain:CASI/Ei) DNA.
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Luty. and Saitcu.N.
Direct Submission
Submitted (29-FEB-2000) Naruya Saitcu, National Institute of
Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Mishima,
Shizuoka 411-8840, Japan (E-mail:nsaitcu@genes.nig.ac.jp,
URL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene Genealogies of 21 Nuclear Genes
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GACTATGTGCATGTCATGCCTAATGTGTGGAAGGCCGTGGTGGCTGACCGGGGTTACCTG
                                                                                                  GAAAAGGCCCTGGAIATGTTCCGGGCACGCTATTCATCTCCAGTCTTCGTGGTTACAAGC
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                  GCAGCCTTCCTACCCGAATGGGTG 1026
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2-alpha-1-fucosyltransferase"
/protein_id="BAB68642.1"
/db_xxef="G1:182982"
/db_xxef="d1:182982"
/db_xxef="d1:1829
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Mus musculus (sub_species:molossinus, strain:MSM/Msf) DNA.
Mus musculus
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Direct Submission
Submitted (29-FEB-2000) Naruya Saitou, National Institute of Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Mishima, Shizuka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp, UKL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Saitou,N.
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/sub_species="molossinus"
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/note="Sec2; Se"
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                          75;
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Score 802; DB 10;
Pred. No. 7.6e-204;
                        0; Mismatches
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90.2%;
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ATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGTTCCTCAAAGTCTTTAAGCCAGAG 1002
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                                                                                                              GCGCCCAICTTCAGGATCAGCCTCCCGGTGTTAGACAGCGACACGGCCAAAAAAATCCCA 402
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of Five Mus musculus subspecies
Unpublished
                                                                                                                                160 TTCACGATCAATTCCATCGGCCGCCTGGGGAACCAGATGGGCGAATATGCTACATTGTTT
                                            GCACTGGCCAGGATGAACGGACGGCTTGCGTTCATCCCCGCATCCATGCACACGCTCTA
                                                              TATGIGGATTCACGGGATACCCGIGCTCTGGACCTTCTACCACACCTGGGCCCAGAG
                                                                                                                                                                                                                                                                                                                                            403 IGGCAGAATIACCAICICAACGACIGGAIGGAGGGAGCGIIACCGCCACAIICCGGGACAC
                                                                                                                                                                                                                                                     TITGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACCACCTGCGCCCAGAG
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963 bp DNA linear ROD 02-Mus musculus FUT2 gene for GDP-L-flucose:beta-D-galactoside 2-alpha-1-flucosyltransferase, partial cds, strain:SWN/Msf. AB039120 GI:15822985
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HDHVREEAOAFLRGLRVNGSOPSTFVGVHVRKGDYVHYMPKVWKGYVADRGYLEKALD
                                         ROD 02-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFRARYSSPVFVVTSNGMAMGRENINWSLGDVVFAGNGIEGSPAKDFALLTQCNHTIM
TIGIFGIWAAYLAGGDTIYLANYTLPDSPFLKIFKPAAAFLPEWM"
285 c 257 g 207 t
                                                                                                                    FUT2; GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase.
Mus musculus (sub_species:domesticus, strain:pgn2) DNA.
Mus musculus
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Mishima,
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                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus FUT2 gene for GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase, partial cds, strain:pgn2.
                                                                                                                                                                                                                        Liu,Y., Kitano,T., Koide,T., Shiroishi,T., Moriwaki,K. and
Saitou,N.
                                                                                                                                                                                                                                                                                                          2 (bases I to 963)
Liu,Y. and Saitou,N.
Direct Submission
Submitted (29-FEB-2000) Naruya Saitou, National Institute
Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, 1
Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp,
URL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="7"
/note="sequence used for primer design based on
Acc#AF064792"
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-2a.bpha-1-fucosyltransferase"
/protein.id="pab68643.1"
/db_xref="G1:15822964"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sub_species="domesticus"
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/organism="Mus musculus"
/strain="pgn2"
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/note="Sec2; Se"
/codon_start=1
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/gene="FUT2"
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/gene="FUT2"
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2 (bases 1 to 963)
Liu,Y. and Saitou,N.
Direct Submission
Submitted (29-FEB-2000) Naruya Saitou, National Institute of
Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, PShizuoka All-8540, Japan (E-mail:insaitou@genes.nig.ac.jp,
URL:http://sayer.lab.nig.ac.jp/, Tei:81-559-81-6790,
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                                                                                                1. .963
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                                                                                    Socation/Qualifiers
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/gene="FUT2"
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Best Local S.
Matches 888
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completed: May 26, 2003, 14:49:14 ne : 3102.72 secs

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(without alignments)
8682.922 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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|---------|---|--------|--------------------|---------------|-------------------|----------------------|--------------------|--------------------|--------------------------|--------------------|---|---|--------------------|------------------|-------------------|-----------|--------------------|--------------------|--|
| CHINGRA |   |        | ID                 |               | AAC67965          | 10000                | MMD2/20/           | AAC67966           | 0000000                  | AMD 2 / 200        | AAV29003                                | 000000000000000000000000000000000000000 | AAV21639           | CCCOSTAGE        | AAV 28323         | ART.64725 | 000                | ABL66311           |  |
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| ancreas cancer<br>ig H transfera | nent of pH | Lpha-1,2  | T DIId I I Z | -filonse-beta | -Alpha-fucosylt | Alpha-fucosyltr | uman H-transfera | H-transfera | H2Kb gene p | alpha 1.2 f | ken beta-a | DP-Fuc:beta-D-ga | in alpha( | encoding | . laevis alr | uman secrete | t alpha    | abbit alphal | t alphal | uma  | oha1- | alpha1- | alphal- | Rabbit alphal-2fuc | Human cDNA clone ( | Human cDNA sequenc | polynuc | polynucleot |          | secrete  | oding no | 00       | polynucle |
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## ALIGNMENTS

AAC67965 standard; cDNA; 1149 BP

RESULT 1 AAC67965 AAC67965;

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Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2calbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease; small cell lung carcinoma; ss.
                                                      Rat hepatoma H35 cell alphal-2fucosyltransferase cDNA.
                                                                                                                                                                                                                                        - 77
                                                                                                                                                                                                                   (PACI") PACIFIC NORTHWEST CANCER FOUND.
                                                                                                                                                                                99WO-US07384.
                                                                                                                                                                                                  99WO-US07384.
                                     (first entry)
                                                                                                                                                                                                                                       Holmes EH, Sherwood AL;
                                                                                                                                                                                                                                                         WPI; 2000-687262/67.
P-PSDB; AAB36104.
                                                                                                                        Rattus norvegicus
                                                                                                                                         WO200064464-A1.
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                                    19-FEB-2001
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The present sequence is given in a specification relating to a rat ganglioside GM_1-specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-3Galbetal-3GalNAc.

Fucalphal-3Galbetal-3GalNAc, a glycolipid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising Fucalphal-2Galbetal-3GalNAc.

The method involves contacting alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoprotein, glycolipoprotein or oligosaccharide having a terminal Galbetal-3GalNAc group. It is also oligosaccharide having a terminal Galbetal-3GalNAc group. It is also begin for synthesis of fucosyl-GM_1 by contacting the protein with glycolipoproteins, glycolipids and oligosaccharides are useful as nutritional compositions and ducosyl-GM_1 is useful for inducing an immunotherapeutic or immunosuppressive action against cancer,
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New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGAATTACCGATGACGACTCAAATGTCCTCGGGAAACACAGAAAGCCCCAGAGATGCGA
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                                                                                                                                                                                                                                                                                                                      neurological disease or small cell lung carcinoma.
                                                                  Claim 10; Fig 5; 91pp; English
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Matches 1149: Conserv
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ACCCTTCCGGATTCTCCGTTCCTCAAAGTCTTTAAGCCAGAGGCAGCCTTCCTACCCGAA 1020
                                                                                                                                                                                                                                                                                                                              CGGTCCCACTTCCACCTCAAGGCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTC 1140
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 CCTAATGTGTGGAAGGGCGTGGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATG
                                                                                ACCTITGGGATTTGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTAC
                       TICCGGGCACGCTATICATCICCAGICTICGIGGITACAAGCAACGGIAIGGCCIGGIGC
                                                                    CGGGAGAACATTAATGCTTCCCGAGGAGACGTGTGTTCGCGGGCAATGGTATTGAGGGG
                                                                                                                 TCGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCATCATGACTATTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat; alphal-2fucosyltransferase; alphal-2fucT; antisense therapy; galactose betal-3n-acetylgalactosamine; Galbetal-3GalNAc; glycolpid; glycolpoprotein; ollgosaccharide; fucosyl-GMi; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GMI;
                                                                                                                                                                                                                                                                      hepatoma H35 cell alphal-2FucT'
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662..1149
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The invention relates to rat GMI-specific alphal-2fucosyltransferase
(alphal-2FucT) enzyme and its corresponding nucleic acid. This nucleic
acid is specific for a carbohydrate moiety found in ganglioside GMI,
a terminal galactose betal-1N-acetylgalactosamine (Galbetal-3GalNAc)
saccharide. Alphal-2FucT DNA is useful for producing rat alphal-2FucT
protein by recombinant techniques. Alphal-2FucT DNA is useful for the
preparative synthesis of fucosyl containing glycolipids, glycoproteins,
glycolipoproteins and oligosaccharide, and for preparing fucosyl-GMI.
Alphal-2FucT DNA is useful for detecting oncogenic transformation which
involves assaying for changes in expression of alphal-2 FucT. Since
alphal-2FucT is activated in cell transformation, antisense sequences
derived from alphal-2FucT DNA is useful for inhibiting, suppressing
or treating cancer. Alphal-2FucT DNA is useful in gene therapy and
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                                                       for producing
                                                 Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for producing GMI-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues
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                                                                                                                      Claim 1; Fig 5; 41pp; English.
2002-121132/16
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1080 1020 1080 900 900 601 AGCCAGCCGAGTACTTTGTGGGTGTCCATGTGCGCCGAGGGGACTATGTGCATGTCATG 660 New rat ganglioside GMI-specific alpha1-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition Rat hepatoma H35 cell alphal-2fucosyltransferase catalytic domain cDNA CCTAATGTGGAAGGGCCTGGTGCCTGACGGGGTTACCTGGAAAAGGCCCTGGATATG CCTAATGTGTGGAAGGCGTGGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATG TICCGGGCACGCIAIICAICICCAGICTICGIGGIIACAAGCAACGGIAIGGCCIGGIGC CGGGAGAACATTAATGCTTCCCGAGGAGACGTGTGTTCGCGGGCAATGGTATTGAGGGG TCGCCAGCCAAGGACTTCGCGCTGCTACCAGTGCAACCACATCATGACTATTGGG 841 TCGCCAGCCAAGGACTTCGCCGCTCACCCAGTGCAACCACCACCATCATTGGG CGGTCCCACTTCCACCTCAAGGCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTC ACCTTTGGGATTTGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTAC ACCTTTGGGATTTGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTAC ACCCTICCGGATTCTCCGTTCCTCAAAGTCTTTAAGCCAGAGGCAGCCTTCCTACCCGAA TGGGTGGGCATCCCTGCCGATCTGTCCCCACTCCTTAAGGCATTAACACCAGCCTGTCCT Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease; (PACI-) PACIFIC NORTHWEST CANCER FOUND AAC67966 standard; cDNA; 1068 BP. lung carcinoma; ss. 99WO-US07384, 95WO-US07384 (first entry) Holmes EH, Sherwood AL; TGATGGGAA 1149 TGATGGGAA 1149 WPI; 2000-687262/67 Rattus norvegicus P-PSDB; AAB36105 WO200064464-A1 23-APR-1999; 23-APR-1999; 19-FEB-2001 02-NOV-2000 1021 1021 1081 1141 781 901 961 961 1081 1141 AAC67966; 199 661 721 901 721 781 **AAC67966** RESULT g ŏ 셤 δy pp pp δ g δ g δŏ qq ŏ Db ŏ Óχ ă

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P-PSDB; AAE16623
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immunotherapeutic for cancer and neurological diseases
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/product= "Rat hepatoma H35 cell alphal-2FucT catalytic
                   CTGCTCACCCAGTGCAACCACCATCATGACTATTGGGACCTTTGGGATTTGGGCTGCC
                                                                                                    TACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat; alphal-2fucosyltransferase; alphal-2FucT; antisense therapy; galactose betal-3N-acetylgalactosamine; Galbetal-3GalNAc; glycolipid; glycoprotein; glycolipoprotein; oligosaccharide; fucosyl-GM1; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GM1; cell transformation; catalytic domain; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat hepatoma H35 cell alphal-2FucT catalytic domain encoding DNA.
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581..1068
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                 The invention relates to rat GMI-specific alphal-2fucosyltransferase
(alphal-2FucT) enzyme and its corresponding nucleic acid. This nucleic
acid its specific for a carbohydrate moiety found in ganglioside GMI,
a terminal galactose betal-3W-acetylgalactosamine (Galbetal-3GalNAc)
saccharide. Alphal-2FucT DNA is useful for producing rat alphal-2FucT
protein by recombinant techniques. Alphal-2FucT DNA is useful for the
preparative synthesis of fucosyl containing glycolipids, glycoproteins,
glycolipoproteins and oligosaccharide, and for preparing fucosyl-GMI.
Alphal-2FucT DNA is useful for detecting oncogenic transformation which
involves assaying for changes in expression of alphal-2 FucT. Since
alphal-2FucT is activated in cell transformation, antisense sequences
derived from alphal-2FucT DNA are useful for inhibiting, suppressing
or treating cancer. Albhal-2FucT DNA is useful in gene therapy and
antisense therapy. The present sequence is at hepatoma H35 cell
calphal-2FucT catalytic domain encoding DNA.
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                                                                                                                                                                                                             93.0%; Score 1068; DB 24; Length 1058; 100.0%; Pred. No. 7.3e-288;
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Claim 2; Fig 3; 41pp; English.
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Matches 1068; Conservative
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CIGCTCACCCAGTGCAACCACCATCATGACTATTGGGACCTTTGGGGATTTGGGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTCTGATGGGAA 1149
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transgenic animal; xenotransplantation; organ transplant; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porcine secretor transferase (FUT2) gene.
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the tissue, especially porcine heart, liver, kidney or pancreas, rendering it more suitable for transplantation, i.e. less immunogenic and of increased immunological acceptability. A claimed method of producing a cell from a donor species that is immunologically acceptable to a recipient species involves reducing levels of carbohydrate on the donor cell that causes it to be recognised as non-self by the recipient by causing a nucleic acid for a glycosyltransferase such as Se to be expressed in the cell. Expression units, such as retroviral packaging or produce cells, containing Se nucleic acids can be used in gene therapy.
                                                                                                                                                                                                                         Score 630.2; DB 19; Length 1043:
Pred. No. 1.1e-165;
0; Mismatches 203; Indels 42;
                                                                                                                                                                                         Sequence 1043 BP; 189 A; 352 C; 306 G; 196 T; 0 other;
                                                                                                                                                                                                                             54.8%;
76.9%;
                                                                                                                                                                                                                                           Best_Local Similarity 76.9
Matches 814; Conservative
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ACCCTTCCGGATTCTCCGTTCCTCAAGTCTTTAAGCCAGAGGCAGCCTTCCTACCCGAA 1020
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                                                                                                                   The present sequence encodes pig secretor used in an example of the present invention. The present invention describes nucleic acids (NA) encoding a chimeric glycosyltransferase. The NAS comprise a caralytic domain of a first glycosyltransferase (GT) and a localisation signal of a second GT, whereby when the NA is expressed in a cell and where the chimeric enzyme is located in a marea of the cell where it is able to compete for substrate with a second GT, resulting in reduced levels of a product from the second GT. The NAS can be used to produce cells and organs with desired glycosylation patterns. Products and methods of the present invention can be used to reduce the levels of undesirable epitopes in cells, issues or organs which may be used in
            TCGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCATCATGACTATTGGG
                                                                ACCITITGGGATITGGGCTGCCTACCIGGCAGGTGGTGATACCATCTACTTAGCCAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycosyltransferases - used for
the surface of cells, useful in
                                                                                                                                                                                                                                                                                                                                                           chimeric; glycosyltransferase; gene therapy;
                                                                                                                                                                     TGGGTGGGCATCCCTGCCGATCTGTCCCCACTCCTTAAG 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "secretor'
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Fig 6; 51pp; English.
                                                                                                                                                                                                                                                  AAV21639 standard; cDNA; 1043
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                                                                                                                                                                                                                                                                                                                                                                         transplantation; ss.
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                                                                                                                                                                                                                                                                                                                                                              secretor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McKenzie IFC,
                                                                                                                                                                                                                                                                                                                                  Pig secretor
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Seguence 1043 BP; 189 A; 352 C; 306 G; 196 T; 0 other;

us-10-040-863-7.rng

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CACCATCATCCACCTCCAGCAGCGAATAGTGAAGCTCCAAQCCCTGTCAGAGAAGGAATT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence encodes the human Sec2 protein of the invention. The DNA encodes a alpha(1,2) fucosyltransferase and is the Secretor alpha(1,2) fucosyltransferase locus, that cross hybridises with the H blood group alpha(1,2)fucosyltransferase gene. The DNA is useful for producing a recombinant human GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase (FUT2) which can be used for genotyping an individual as a secretor or nonsecretor as it is known that nonsecretors homozygous for a mutant allale of the FUT2 gene that has a stop codon in the position corresponding to amino acid 143.
                                                                                                                                                                                                                          Sec2; alpha(1,2) fucosyltransferase; H blood group; secretor genotyping: GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase; human; FUT2; nonsecretor genotyping; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 CGCCCAGGTTCCTTTCTCCTCTGGCCCACTTCCTCTTTGTCTTCGTGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding fucosyltransferase enzyme - useful for producing recombinant enzyme and genotyping person as secretor or nonsecretor
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                 987 TGGATTGGGATCGAGGCAGACCTGTCCCCACTCCTTAAG 1025
TGGGTGGGCATCCCTGCCGATCTGTCCCCACTCCTTAAG 1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Column 45-50; 55pp; English.
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64..1095
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                                                                                                                                                                                              Human Sec2 coding sequence
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(KELL/) KELLY R J.
(LENNON G.
(LOWE/) LOWE J B.
(ROUQ/) ROUQUIER S.
                                                                                                                                                                 (first
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P-PSDB; AAW69332.
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                                                                                                                                                                                                                                                                                                                                                                         GGACGGCTTGCGTTCATCCCCGCATCCATGCACACGCTCTAGCGCCCATCTTCAGGATC
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                                                                                               ArgCICAGCATGCAGCCATCTTCTTCCCCACGGGTCCCTTCATCCTTTGTCTTC
                                                                                                                                                             ACGGCTTCCACCATATTTCACCTTCAGCAGGATGGTGAAGATTCAACCCACGT-----
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              Length 1043;
                                          Indels
              DB 19;
           Score 630.2; DB 19
Pred. No. 1.1e-165;
); Mismatches 203;
                                       0;
           54.8%;
76.9%;
                                     814; Conservative
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Best Local (
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Gaps

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(first entry)

15-MAY-2002

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338 368

279 GGGAACCAGATGGGCGAGTACGCCACTATACCCCTGGCCAAGATGAACGGGCGGCC

458

GGTGTTACACAGCGACACGGCCAAAAAGATCCCATGGCAGAATTACCATCTCAACGACTG 428

TGCGTTCATCCCCGCATCCATGCACACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCC

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518 548

235

129 ACCGATGACGACTCAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGACGGGACAG 188

192 GCAGATACCAGTGCTAGCCTCAACATCAAAGGCACTGGGACCCA---------CGAGCAGCATGGGAATGGAGGGGGGGGGGATGTTCACGATCAATTCCATTGGCCGGCT 

189 236

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ABL64735;

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818

878

938 896

758 788

608 638 668 698 728

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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                                                                                                                                                                        Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         တ်
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                                                                                                                           related gene sequence SEQ ID NO:3072
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200005-209531P.
200005-233617P.
200005-234009P.
200005-234009P.
200005-234052P.
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2000US-237425P.
2000US-237598P.
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22-SEP-2000;
25-SEP-2000;
                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                           Lung cancer
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Soppet DR,
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                                                                                                                                                                                                                                                                             ds.
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oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarichnoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, seurcendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                          The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical expent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (1) of a signature gene set, where (1) comprises a sequence (8) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (8), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of canners used as colon, breast, stomach, lung, thyroid,
Claim 1; SEQ ID 3072; 44pp; English
\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset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Sequence 3088 BP; 723 A; 839 C; 798 G; 728 T; 0 other;

|  | 1;      | 1 88   | ۱<br>ک   | 128  | 239   | 188  | 283   | 248  | 326                                    | 308  | 386                              | 368   | 446  | 428   | 206  | 488   | 566  | 548  | 626   | 809  | 989   | 668  | 746   | 728   | 808  |
|--|---------|--|--|--|---|--|---|--|--|--|----------------------------------|---|--|---|--|---|--|--|---|--|---|--|---|---|--|
| Ouery Match 53.3%; Score 612.6; DB 24; Length 3088; Best Local Similarity 73.8%; Pred. No. 1.4e-160; |         | CGCCCAAGTTCCTTTCTCCTTTCCTCTAGCCCACTICCTCATCTTTGTCTTCGTGACTTC | CGIICAGAIGCCIIICCCIIIICCCAIGGCCCACIICAICIICIIIGICIIIACGGITIC | CACCATCATCATCCACCTCCAGGGGGAATAGTGAAGGTCCAACCCCTGTCAGAGAAGGAATT | CACTATATTTCACGTTCAGCAGCGGCTAGCGAAGATTCAAGCCATGTGGGGAGTTACCGGT | ACCGATGACGACTCAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGACGGGACAG | GCAGATACCAGTGCTAGCCTCAACATGAAGGCACTGGGACCCA | CGAGCAGCATGGGAATGGAGCTGCGGGGCATGTTCACGATTCCATTGGCGGGCT | GCCAGCTCAGGGGATGTGGACGATCAATGCAGCCGCCT | GGGGAACCAGATGGGCGAATACGCCACACTCTTTGCACTGGCCAGGATGAACGGACGG | GGGGAACCAGATGGGGGAGGACCCCACACTGT | TGGGTTCATCCCCGCATCCATGCACAACGCTCTAGCGCCCCATCTTCAGGATCAGCCTCCC | CGCCTTCATCCCGGCCCAGATGCACAGCACCTGGCCCCCCATCTTCAGAATCACCCTGCC | GGTGTTACACAGGCCAAAAAGATCCCATGGCAGAATTACCATCTCAACGACTG | GGTGCTGCACACGCCCAGCAGCACGATCCCCTGGCAGAACTACCACCTGAACGATC | GATGGAGGATTACCGCCACATTCCGGGACACTTTGTGCGCTTCACGGGATACCCGTG | GATGGAGGAGGATACCGCCACTTCCCGGGGGAGTACGTCCGCTTCACCGGCTACCCTG | CTCCTGGACCTTCTACCACCACCTGCGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGA | CICCTGGACCTTCTACCACCACCTCCGCCAGGAGATCCTCCAGGAGTTCACCTGCACGA | CCACGTGCGGGAGGAGGCCCAGGCCTTCCTGCGTGGTGTGAATGGGAGCCAGCC | CCACGTGCGGGAGGAGGCCCAGAAGTTCCTGCGGGGCCTGCTGGAGGGGAGCCGGCC | GAGTACTTTTGTGGGTGTCCATGTGCGGGGGGCGTATGTGCGATGTGCTAATGT | GGGCACCTTTGTAGGGGTCCATGTTCGCCCGAGGGGACTATGTCCCATGTCATGCCCAAAAGT | GTGGAAGGCCTGGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGCC | GTGGAAGGGGGTGGTGGCCGACCGGCGATACCTACAGCAGCCCCTGGACTGGTTCCGAGC |
| ry Match<br>t Local  | 80      | 9 120  | 7  | 69   | 180   | 129  | 240   | 189  | 284                                    | 249  | 327                              | 309   | 387  | 369   | 447  | 429   | 507  | 489  | 567   | 549  | 627   | 609  | 687   | 699   | 747  |
| uery M   | latches |  |  |  |   |  |   |  |  |  |                                  |   |  |   |  |   |  |  |   |  |   |  |   |   |  |
| 3 3 11   | 4       | لام بو   | G C  | δŽ   | qq  | ΩŽ   | qa  | QY   | Op                                     | δŽ   | qq                               | Qy  | qq   | QY  | qq   | QΫ  | qa   | Qy   | qq  | Qγ   | qq  | ΟY   | qq  | Qy  | qa   |

2000US-235720P

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1047 CGACTCCCCTTTCCTCAAAATCTTTAAGCCAGAGGCAGCCTTCCTGCCGGAGTGGACAGG 1106
                                                                                                                                                                                                                            1029 CATCCCTGCCGATCTGTCCCCACTCCTTAAGGCATTAACACCAGCCTGTCCTCGGTCCCA 1088
                                                                                                                                                                                                                                                 1107 GATTGCCGCAGACCIGTCCCCCTTACTCAAGCACTAATGCTGGCCCATTCTTTGAGACCT 1166
             729 ACGCTATICATCICCAGICTICGIGGITACAAGCAACGGIATGGCCIGGIGCCGGGAGAA 788
                                                                                       CAAGGACTTTGCGCGCTGCTCACCCAGTGCAACCACCATCATGACTATTGGGACCTTTGG 908
                                                                                                   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                           CATTAATGCTTCCCGAGGAGACGTGTGTTCGCGGGCAATGGTATTGAGGGGTCGCCAGC
                                                        GATTTGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTACATTCC
                                                                                                                                                                               -71
                                                                                                                                                                                                                                                                                                                                                                                                                         Lung cancer related gene sequence SEQ ID NO:4648.
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                                                                                                                                                                                                                                                                                             1167 TTTCTCCTTCTCC 1181
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20000S-234039P
20000S-234034P
20000S-234052P
20000S-234509P
20000S-234567P
20000S-234967P
20000S-234967P
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2000US-209531P.
2000US-233133P.
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2000US-235134P.
2000US-235280P.
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2000US-235638P.
2000US-235711P.
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20 - SEP - 2000;
20 - SEP - 2000;
20 - SEP - 2000;
22 - SEP - 2000;
25 - SEP - 2000;
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27-SEP-2000;
27-SEP-2000;
27-SEP-2000;
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us-10-040-863-7.rng

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The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical expension by the method involves exposing cells to a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is inflicient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
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03-0CT-2000; 2000US-23759F.
03-0CT-2000; 2000US-23759F.
03-0CT-2000; 2000US-237604F.
03-0CT-2000; 2000US-237606F.
03-0CT-2000; 2000US-237608F.
01-NOV-2000; 2000US-24867F.
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2000US-236111P.
2000US-236842P.
2000US-236891P.
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2000US-237295P.
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2000US-236034P.
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28-SEP-2000;
28-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
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PPR R R PPR PP
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CACCATCATCCACCTCCAGCAGCGAATAGTGAAGCTCCAACCCCTGTCAGAGGAAGTT 128 129 ACCGATGACGACTCAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGACGGGACAG 188 CGAGCAGCATGGGAAATGGAGGAGCTGCGGGGCATGTTCACGATCAATTCCATTGGCCGGCT 248 9 CGCCCAGGTTCCTTTCTCCTTTCCTCTGGCCCCACTTCCTCATCTTTGTCTTCGTGACTTC .80 CACTATATTTCACGTTCAGCAGCGGCTAGCGAAGATTCAAGCCAIGTGGGAGTTACCGGT 53.3%; Score 612.6; DB 24; Length 3088; larity 73.8%; Pred. No. 1.4e-160; Conservative 0; Mismatches 254; Indels 33; GCAGATACCAGTGCTAGCCTCAACATCAAAGGCACTGGGACCCA---Best Local Similarity Matches 808; Conserv δ 120 69 g δ qq δŽ g

Pancreas cancer related gene sequence SEQ ID NO:8363.

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1047 CGACTCCCCTTTCCTCAAAATCTTTAAGCCAGAGGCAGCCTTCCTGCCGGAGTGGACAGG 1106
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                                TGGGTTCATCCCCGCATCCATGCACACGCTCTAGCGCCCCATCTTCAGGATCAGCCTCCC
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Claim 1; SEQ ID 8363; 44pp; English.  $\mathbb{Z}$ 

Humar, cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;

Homo sapiens.

WO200194629-A2

13-DEC-2001

30-MAY-2001;

05-JUN-2000;

2000US-234509P. 2000US-234567P. 2000US-234009P 2000US-234052P. 2000US-234923P. 2000US-233133P 2000US-233617P 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 22-SEP-2000; 18-SEP-2000;

2000US-235134P. 2000US-235280P. 2000US-234924P 2000US-235077P 2000US-235082P 22-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000;

26-SEP-2000; 2000US-225634P.
26-SEP-2000; 2000US-225634P.
27-SEP-2000; 2000US-225634P.
27-SEP-2000; 2000US-225634P.
27-SEP-2000; 2000US-235840P.
28-SEP-2000; 2000US-235863P.
28-SEP-2000; 2000US-236034P.
28-SEP-2000; 2000US-236034P.
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28-SEP-2000; 2000US-236034P.
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29-SEP-2000; 2000US-236111P.
29-SEP-2000; 2000US-23634P.
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29-SEP-2000; 2000US-23634P.
29-CCT-2000; 2000US-237348P.
02-CCT-2000; 2000US-237348P.
03-CCT-2000; 2000US-23736P.
03-CCT-2000; 2000US-23736P.
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03-CCT-2000; 2000US-23756P.
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03-CCT-2000; 2000US-23756P.
03-CCT-2000; 2000US-23756P.
03-CCT-2000; 2000US-23760P.
01-NOV-2000; 2000US-23766P.

(AVAL-) AVALON PHARM.

Horrigan Endress G, Ebner R, Carter KC, Augustus M, Weaver Z; WPI; 2002-188264/24. Young PE, I

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in

expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent which result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, and Wilm's tumour. Gaps DB 24; Length 3088; Score 612.6; DB 24; L.L., Pred. No. 1.4e-160; Indels Sequence 3088 BP; 723 A; 839 C; 798 G; 728 T; 0 other; 0; Mismatches 53.3%; 73.8%; Best\_Local Similarity 73.8
Matches 808; Conservative Query Match Best Local S 55555555555555555888

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129 ACCGAIGACGACTCAAATGTCCTCGGGAAACACAGAAAGCCCCAGAGATGCGACGGGACAG 240 GCAGATACCAGTGCTAGCCTCAACATCAAAGGCACTGGGACCCA----189

308 --------GCCAGCTCAGGGGATGTGGACGATCAATGCAATAGGCCGCCT 249 GGGGAACCAGAIGGGCGAATACGCCACACTCTTTGCACTGGCCAGGAIGAACGGACGGCT CGAGCAGCATGGGAATGGAGAGCTGCGGGGCATGTTCACGATCCAATTCCATTGGCCGGCT 284

386 446 GGGGAACCAGATGGGCGAGTACGCCACACTGTACGCCCTGGCCAAGATGAACGGGCGGCC TGCGTTCATCCCCGCATCCATGCACACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCC 387 327 309 q g ŏ

428 GGTGTTACACACGGCCAAAAAAATCCCATGGCAGAATTACCATCAACGACTG 447 369 Qχ qq

488 566 GATGGAGGAGCGTTACCGCCACATTCCGGGACACTTTGTGCGCTTCACGGGATACCCGTG GATGGAGGAGAATACCGCCACTTCCCGGGGGAGTACGTCCGCTTCACCGGCTACCCCTG CTCCTGGACCTTCTACCACCACCTGCGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGA 507 489 429 g δy δ

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GTGGAAGGGCGTGGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGC 699 747

866 ACGCTATTCATCTCCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAA 807 TCGCTACACTCCCTCATCTTCGTGGTCACCAGTAATGGCATGGCCTGGTGGGGAGAA 729

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CATCCCTGCCGATCTGTCCCCACTCCTTAAGGCATTAACACCAGCCTGTCCTCGGTCCCA 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes pig H transferase used in an example of the present invention. The present invention describes nucleic acids (NA) encoding a chimneric glycosyltransferase. The NAs comprise a catalytic domain of a first glycosyltransferase (GT) and a localisation signal of a second GT, whereby when the NA is expressed in a cell and where the chimneric enzyme is located in an area of the cell where it is able to
                                                                                                            CAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCATCATGACTATTGGGACCTTTGG
                                                           CATTAATGCTTCCCGAGGAGACGTGGTGTTCGCGGGCAATGGTATTGAGGGGTCGCCAGC
                CATTGACACCTCCCACGGTGATGTGGTTTGCTGGCGATGGCATTGAGGGCTCACCTGC
                                                                                              GATTTGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTACACCTTCC
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compete for substrate with a second GT, resulting in reduced levels of a product from the second GT. The NAs can be used to produce cells and organs with desired glycosylation patterns. Products and methods of the present invention can be used to reduce the levels of undesirable epitopes in cells, tissues or organs which may be used in
                                                                                                                                                                                                                             GCICTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGGGACACGGCCAAAAAG
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                                                                                                                                              Score 423.8; DB 19; Length 1098; Pred. No. 4.7e-108; 0; Mismatches 252; Indels 5;
                                                                                                                Sequence 1098 BP; 181 A; 367 C; 312 G; 238 T; 0 other;
                                                                                transplantation or gene therapy.
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517 CCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAGGCCCAGGCCCTTC
423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGCCCGAGGATTATGCCCACTTAAAG
                             GGACACTITIGIGCGCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACCACCTGCGC
                                                                                                                   543 GAGCAGATCCGCAGCTACACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Swine alpha-1,2-fucosyltransferase 1 encoding DNA.
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1083 CTCCAGATG 1091
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                                                                                                                                                      Swine alpha(1,2) fucosyltransferase; FUT1; Escherichia coli; resistant; E. coli-associated intestinal disorder; E coli infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes swine alpha(1,2) fucosyltransferase (FUT1). The specification describes methods relating to Escherichia coli-resistant swine. One of the methods for identifying a swine resistant to E. coli-associated intestinal disorders, comprises determining whether the base at 307 of alpha(1,2) fucosyltransferasel gene (FUT1) is adenine (sic), in which case the swine are resistant. The porcine FUT1 polymorphisms can be used to develop drugs for the treatment of swine having E. coli-associated disease. The methods can also be used in breeding programmes to identify swine with resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCTGGCCCTGGCGCACTCAACGCCCCCAGGCCTTCATCCAGCCTGCCATGCACGCC
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                                                                                                                          Fragment of pHT83xF encoding swine alpha(1,2) fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.9%; Score 423.8; DB 20; Length 1269; 69.6%; Pred. No. 5e-108; ative 0; Mismatches 252; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases - using PCR-RFLP to assay for polymorphisms in the alpha(1,2) fucosyltransferase 1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 other;
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                                    AAX15872 standard; DNA; 1269
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Best Local Similarity 69.6
Matches 591, Conservative
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          RESULT 12
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                                                                                                                                                                                                                                                                                                                                     resistant to intestinal colonisation by E. coli. The method comprises determining whether a genetic polymorphism associated with resistance to colonisation is present in a swine sample, and then inferring that the swine is resistant if it is homozygous for the polymorphism. The method uses the swine alpha-1,2-fucosyltransferase (FUT1) polymorphism. The present sequence encodes swine FUT1. The method enables the breeding of swine that are resistant to E. coll-related diseases. This method comprises breeding swine that have a genetic polymorphism in the FUT1 gene. Nor particularly, the identification method identifies swine that are resistant to E. coll-related intestinal disorders if, in a sample taken, the only nitrogen base at residue 307 in the FUT1 gene is adenine and the assay itself is used as a basis for a kit, applied to swine of any age, in detecting polymorphisms associated with E. coli FNB receptors. The polymorphisms are useful in developing drugs to treat source with the normal enzyme and prevent it forms the may interfere with the normal enzyme and prevent it forms the may interfere with the normal enzyme and prevent it
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from producing the intestinal receptor for F18. The detection of polymorphic markers in the method disclosed enables the detection and treatment of E. coli-related intestinal diseases in swine, where there has been no success using antibiotics due to unsuccessful prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGGCGAATACGCCACA
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                                                                                                                                                                                                                                                                                                                        A method has been developed for the identification of swine that are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New method of identifying swine that are resistant to intestinal colonisation by Escherichia coli - comprises use of genetic polymorphic markers, used for breeding swine resistant to Escherichia coli-related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20; Length 1269;
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                                 (BIOT-) BIOTECHNOLOGY RES & DEV CORP. (SWTE-) SWISS FEDERAL INST TECHNOLOGY ZURICH. (USDA ) US SEC OF AGRIC.
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Pred. No. 5e-10
0; Mismatches
                                                                                                                                                                                                                                                                                    Claim 6; Fig 1; 35pp; English
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69.68;
97US-0047181
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                                                                                                        Vogeli P;
                                                                                                                                          WPI; 1999-059746/05.
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Best Local Similarity
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                                                                                                        Bosworth BT,
 20-MAY-1997;
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603 CTGAGTCASTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGGTCCAC 662
                                                                                                                                                                                     GTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCCCGAGGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUT1; pig; polymorphism; ss.
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/transl_except= (pos:726..728,
replace(315,A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pig alpha-1-2 fucosyltransferase FUT1 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-1-2 fucosyltransferase;
Escherichia coli; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ94417 standard; DNA; 1269
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us-10-040-863-7.rng

Page 15

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This is the nuclectide sequence of the pig FUTI gene encoding alpha-1-2 fucosyltransferase (see AAY9302). A polymorphism at position 307 of the conding region is associated with susceptibility to FIB Escherichia coli colonization; pigs homozygous for adenine at position 307 are resistant to colonization, while heterozygous canimals and animals homozygous for quantine at position 307 are resistant to colonization. A claimed method for improving weight useptible to colonization. A claimed method for improving weight resistant to E. coli colonization and feeding these animals high levels of plant-based protein concentrate. A claimed method for preventing FIB E. coli colonization in swine, especially swine that are genetically susceptible to FIB E. coli colonization, involves replacing some or all of the plant-based proteins in the diet with are genetically susceptible to FIB E. coli colonization, involves replacing some or all of the plant-based proteins in the diet with useful for developing drugs to treat swine that have E. coli associated disease. The polymorphism in the FUTI gene is also associated disease. The polymorphism can be detected using
                                                  Improving weight gain in swine using swine genetically resistant
Escherichia coli and feeding swine high levels of plant based protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 252;
                                                                                                                                                          Disclosure, Fig 1; 33pp; English.
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Matches 591; Conservative
P-PSDB; AAY79302
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36.9%; Score 423.8; DB 21; Length 1269; 69.6%; Pred. No. 5e-108; .; 9 Indels

GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA 276 456 576 CTCTTTGCACTGGCCAGGATGAACGGACGGCTTGCGTTCATCCCCGCATCCATGCACAAC 336 422 543 GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAAGGCCCCAGGGGGTA 602 662 722 CGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCTTC 750 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC Crecredeceracinearceaccecagecericarceaccineargecarece GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCCGAGGTAGACAGGCAC ATCCCATGGCAGAATTACCATCTCAACGACTGGATGGAGGAGCGTTACCGCCACATTCCG CCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAGGAGGCCCAGGCCTTC CTGCGT-----GGTCTGCGGGTGAATGGGAGCCAGCCGAGTACTTTTGTGGGTGTCCAT GGACACTITIGIGGGCTICACGGGATACCCGTGCTCCTGGACCTICTACCACCACCTGCGC 517 277 303 363 397 423 457 577 603 631 663 691 ŏ q g Dp Op. g qq QQ 23 ŏ ŏ ŏ g ŏ 07 QΥ ã

GGCCGTTACCTCCAGCAGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTT 782

GTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCCCGAGGAGAC 

751

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811

GIGGIGITCGCGGCCAATGGIATTGAGGGGTCGCCAGCCAAGGACTTCGCGCTGCTCACC 870

1082 Feeding swine genetically susceptible to F18 Escherichia colicolonization with a low plant protein based diet increases weight gain and lowers intestinal disease associated with E. coli infection This sequence represents the swine alpha (1,2) fucosyltransferase (FUT1) gene. A FUT1 gene in which there is a base other than adenine at position 307, may be used for improving weight gain in swine that are genetically susceptible to F18 Escherichia coli. The weight gain may be activated by feeding a diet of at least 40% animal based proteins. The feeding method is used to control F18 E. coli associated intestinal disease in swine. CAGTGCAACCACACCATCATGACTATTGGGACCTTTGGGATTTGGGCTGCCTACCTGGCA 1023 TITABACCCGAGGCTGCCTICCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCICCA GGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGTTCCTCAAAGTC Gene; pig; swine; alpha (1,2) fucosyltransferase; FUT1; weight gain; F18; Escherichia coli; ss. . Ш "Confers resistance to F18 BIOTECHNOLOGY RES & DEV CORP. US SEC OF AGRIC. Location/Qualifiers 9..1106 Claim 1; Column 13-18; 9pp; English. Wiseman B; BP. "FUT1" AAI72831 standard; cDNA; 1269 /\*tag= b /phenotype= 98US-0151592 97US-047181P /product= "
315 (first entry Ridpath J, CTCCTTAAG 1059 CTCCAGATG 1091 WPI; 2002-391652/42. P-PSDB; AAB47995 18-SEP-1998; 20-MAY-1997; Bosworth B, US6355859-B1 22-JUL-2002 Sus scrofa FUT1 CDNA 843 871 1051 1083 931 991 AAI72831; mutation (BIOT-) (USDA AAI7283 qq Db g δX õ ă QY qq 

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963 GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATC 1022
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                                                                                                                                                   422
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                                                                                                        243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
                                                                                                                                                                                         337 GCTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGCGACACGGCCAAAAAG 396
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                                                                                                                                  277 CTCTTTGCACTGGCCAGGATGAACGGACGGCTTGCGTTCATCCCCGCATCCATGCACAAC
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                                                                              217 GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA
                                                     Gaps
                        Score 423.8; DB 24; Length 1269;
Pred. No. 5e-108;
0; Mismatches 252; Indels 6;
Sequence 1269 BP; 219 A; 414 C; 361 G; 275 T; 0 other;
                      n
Similarity 69.6%;
31; Conservative
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                        Query Match
Best Local Simil
Matches 591;
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Patent No. 6329170

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 7
US-09-298-886-114
US-09-298-886-115
US-09-298-886-27
US-08-997-080-113
US-08-997-080-113
US-09-095-855-113
US-09-095-855-113
US-09-095-855-113
US-09-095-855-113
US-09-095-855-1159
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US-09-208-886-28
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Pred. No. 0;
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  US-09-298-886-7
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Best Local Similarity
Matches 1149; Conserv
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US-08-675-773B-4

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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
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US-09-298-886-23
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US-09-298-886-20
                                                                                                                                                                                                           hits satisfying chosen parameters:
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APPLICANT: ETIC H. Holmes et al.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GAL-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT APPLICATION NUMBER: US/09/298,886
SURRENT FILING DATE: 1999-04-26
SUFTWARE: PATCHIN VOET: 2.0
SUFTWARE: PATCHIN VOET: 2.0
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Patent No. 6329170
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100.0%; Pred. No. 1.7e-301;
Live 0; Mismatches 0;
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; NAME/KEY: CDS
; LOCATION: (1)..(1062)
US-09-298-886-9
                                                            Best Local Similarity
Matches 1068; Conserv
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TITLE OF INVENTION: 2-ALBHA-L-FUCOSYLIRANSFERASES, DNA SEQUENCES ENCODING TITLE OF INVENTION: SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF TITLE OF INVENTION: GENOTYPING A PERSON
COMMERO FOR SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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28-FEB-1995
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APPLICATION NUMBER: US/08/39
FILING DATE: 28-FFB-1995
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
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APPLICANT: LENNON, GREGORY
APPLICANT: ROUGUIER, SYLVIE
APPLICANT: GICRGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
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(703) 413-2220
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                                                                                                                                                                                                                                                           APPLICANT: SANDELLAN:
APPLICANT: SANDELLAN G. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
CURRENT PILLE OF 1909-06-11
PRIOR APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DAIE: 1999-06-11
PRIOR PELING DAIE: 1999-08-22
PRIOR APPLICATION NUMBER: PCI/AU97/00540
PRIOR FILING DAIE: 1996-08-23
PRIOR PILING DAIE: 1996-08-23
SUMMER OF SEC ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                          GCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTCTGATGGGAA 1149
                                                                                                                            Length 1043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 630.2; DB 4;
Pred. No. 5.5e-174;
0; Mismatches 203;
                                                                                                                                                                                                                 Sequence 5, Application US/09254077A Patent No. 6399758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.8%;
76.9%;
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Best Local Similarity 76.9
Matches 814; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA; ORGANISM: Sus scrofa US-09-254-077A-5
                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                       US-09-254-077A-5
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849 CAAGGACTICGCGCTGCTCACCCAGTGCAACCACCATCATGACTATTGGGACCTTTGG 908
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Patent No. 2807732
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                 LOWE, JOHN B
LENNON, GREGORY
                                                                                                                                                                                                                                                                ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STRANDEDNESS: double
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US-08-395-800A-1
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                                                                                                                                                                                                                                34;
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                                                                                                                                                                                               Score 613.8; DB 1;
Pred. No. 4.5e-169;
0; Mismatches 242;
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 2115 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear TOPOLOGY: linear MILECULE TYPE: DNA (genomic)
                                                                                                                                                                                               Query Match 53.4%;
Best Local Similarity 74.7%;
Matches 813; Conservative
                                                                                                                                                  64..1092
                                                                                                                                    ), NAME/KEY: CDS
; LOCATION: 64..
US-08-395-800A-7
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APPLICANT: LENNON, GREGORY
APPLICANT: ROUGULER, SYLVIE
APPLICANT: GLORGI, DOMINIQUE
APPLICANT: GLORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
TITLE OF INVENTION: 2-ALPHA-L-FUCOSE: BETA-D-GALACTOSIDE
TITLE OF INVENTION: 2-ALPHA-L-FUCOSYLTRANSPERASES, DNA SEQUENCES ENCODING THE
TITLE OF INVENTION: GROUTYPING A PERSON
UNMBER OF INVENTION: GROUTYPING A PERSON
CORRESPONDENCE ADDRESS: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      1029 CAICCCTGCCGATCTGTCCCCACTCCTTAAGGCATTAACACCCAGCCTGTCCTCGGTCCCA 1088
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STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/395,800A
FILING DATE: 28-FEB-1995
CLASSIFICATION: 435
TELECOMMUNICATION: 1703 413-3000
TELEFRAX: (703) 413-3200
TELEFRAX: (703) 413-3200
TELEFRAX: (703) 413-220
TELEFRAX: 1485 OPAT UR
SEQUENCE CHARACTERISTICS:
LENGTH: 1144 Dase Pairs
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Matches 642; Conserv
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us-10-040-863-7.rni

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Similarity
     LENGTH: 1269
TYPE: DNA
ORGANISM: Swine
                                            NAME/KEY: CDS
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NO 1
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GENERAL INPORMATION:
APPLICANT: Bidsparth, Julia
APPLICANT: Ridsparth, Julia
APPLICANT: Wisceman, Barry
TITLE OF INVENTION: INTERACTIONS BETWEEN GENOTYPE AND DIET IN SWINE THAT
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        CTGCGGGGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATAC
                 CGGGAGGACCTGTTCACTATCAACTCCAAGGGCCGCCTGGGGGAACCAGATGGGCGAGTAC
                                                      CACAACGCTCTAGGGCCCATCTTCAGGATCAGCTCCCGGTGTTACACAGGGACACGGCC
                                                                                                 CACAGCAGGGTGGCCCCCATCTTCAGAATCACCCTGCCGGTGCTGCACAGCGCCACGGCC
                                                                                                                  CTGCGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAGGAGGCCCAG
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                                           GCCACACTCTTTGCACTGGCCAGGATGAACGGACGGCTTGCGTTCATCCCCGCATCCATG
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FILE REFERENCE: 21419-90119
CURRENT APPLICATION WUMBER: US/09/151,592
CURRENT FILING DATE: 1999-09-18
NUMBER OF SEO ID NOS: 4
SOFTWARE: Patentin Ver. 2.0

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                                                                                                                        Gaps
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                                                                                  Length 1269;
                                                                                                                        Indels
                                                                                    DB 4;
                                                                                                                      252;
                                                                                  Score 423.8; DB 4;
Pred. No. 7.9e-114;
                                                                                                                      0; Mismatches
                                                                                    36.9%;
                                                                                                                    591; Conservative
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                                ; OTHER INFORMATION: FUT1
US-09-151-592-1
LOCATION: (9)..(1103)
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                       35.5%; Score 408.2; DB 1;
68.7%; Pred. No. 2.6e-109;
Live 0; Mismatches 258;
                                                                                       Journal of Biological Chemistry
                                                                                                                                                                                                                                                                                                                      RELEVANT RESIDUES IN SEQ ID NO:
                              V.P. Rajan, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 68.7
Matches 579; Conservative
PUBLICATION INFORMATION:
                                                                                                                                                                        11158 - 11167
                                                                                                                                                                                                                              DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
                                                                                                                                                                                                1989
                              AUTHORS:
TITLE:
                                                                                 JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                 US-08-208-889A-1
                                                                                                                                          ISSUE:
PAGES:
DATE: 1
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OTHER INFORMATION: The encoded product of nucleotide SEQ ID NO:
OTHER INFORMATION: 1: is the enzyme, GDP-L-fucose--D-galactoside 2-alpha-fucosy
OTHER INFORMATION: which has the amino acid sequence described in SEQ. ID NO:1:.
OTHER INFORMATION: is responsible for the synthesis of 2'-fucosyllactose.
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                                                                                                                           Sequence 1, Application US/0820889A
Patent No. 5750176
GENERAL INFORMATION:
APPLICANT: Prieto, P., Smith, D., Cummings, R., Kopchick, J., Mukerji, I APPLICANT: Prieto, F., Pierce, J.
TITLE OF INVENTION: Transgenic Production of Oligosaccharides and TITLE OF INVENTION: Glycoconjugates
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMEDIATE SOURCE: Human Epidermal Carcinoma Cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: Entire amino acid sequence provided. ORIGINAL SOURCE: Human Epidermal Carcinoma Cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: No. 5750176 applicable TELECOMMUNICATION INVENSATION:
TELEPHONE: (614) 624-7080
TELEFAX: (614) 624-3074
TELEFAX: No. 5750176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WordPerfect Version 6.0a CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,889A FILING DATE: 09-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSE: Donald O. Nickey
ADDRESSE: ROSS Products Division
ADDRESSE: Abbort Laboratories
STREET: 625 Cleveland Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America
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Nucleic acid
EDNESS: Single
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COMPUTER READABLE FORM:
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DEVELOPMENTAL STAGE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Columbus
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TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
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                                                                                                            US-08-208-889A-1
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Journal of Biological Chemistry
                                                                                                                                                                                                                           PUBLICATION DATE: RELEVANT RESIDUES IN SEQ ID NO:
           OTHER INFORMATION: The encode OTHER INFORMATION: I. is the OTHER INFORMATION: which has OTHER INFORMATION: is respons PUBLICATION INFORMATION: AUTHORS: V.P. Rajan, et al. TITLE:
IDENTIFICATION METHOD:
                                                                                                                                                             PAGES: 11158 - 11167
DATE: 1989
DOCUMENT NUMBER:
                                                                                                                 JOURNAL: Jour
VOLUME: 264
ISSUE:
                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                            APPLICANT: Prieto, P., Smith, D., Cummings, R., Kopchick, J., Mukerji, P., APPLICANT: Moremen, K., Pierce, J.
TITLE OF INVENTION: Humanized Milk
CORRESPONDENCE: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloned cDNA representing the product of a human genomic DNA segment GDP-L-fucose- -D-galactoside 2-alpha-fucosyl-transferase
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:MMEDIATE SOURCE: Human Epidermal Carcinoma Cell line
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ANTI-SENSE:
FRAGMENT TYPE: Entire amino acid sequence provided.
ORIGINAL SOURCE: Human Epidermal Carcinoma Cell line
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS Version 6.21 SOFTWARE: WORDEATED FISSOFT VERSION 6.0a CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/433,271 FTLING DATE: 02-MAY-1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,122
FILING DATE: 09-MAR-1994
CLASSIFICATION:
TELECOMMUNICATION:
TELEPHONE: (614) 624-3074
TELEFAN: (614) 624-3074
TELEFAN: No. 58916986
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
                                                                                                                                                                                                                                        Donald O. Nickey
ROSS Products Division
                                                                                                                                                                                                                                                                                                                                United States of America
                                                                                                                                                                                                                                                                       Abbott Laboratories
                                                                                                                Sequence 1, Application US/08433271
Patent No. 5891698
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    625 Cleveland Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1155 base pair:
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Cloned CDI
MOLECULE TYPE: Cloned CDI
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CHROMOSOME/SEGMENT:
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DEVELOPMENTAL STAGE:
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IISSUE TYPE:
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CLONE:
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CITY: CO
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                                                                                   RESULT 8
US-08-433-271-1
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HOD: DNA sequencing and restriction analysis
The encoded product of nucleotide SEQ ID NO:
1: is the enzyme, GDP-L-fucose- -D-galactoside 2-alpha-fuc
which has the amino acid sequence described in SEQ. ID NO:
is responsible for the synthesis of 2'-fucosyllactose.
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2-ALPHA-L-FUCOSYLTRANSFERASES, DNA SEQUENCES ENCODING THE SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
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                                                                                                     GGACACTITGTGCGCCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACCACCTGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LONE, JOHN B
APPLICANT: LENNON, GREGORY
APPLICANT: ROUGUIER, SYLVIE
APPLICANT: ROUGUIER, SYLVIE
APPLICANT: RELLY, ROBERT J
TITLE OF INVENTION: GDP-L-FUCOS
TITLE OF INVENTION: 3-ALPHA-L-F
TITLE OF INVENTION: GROUTPING
NUMBER OF SEQUENCES: 22
CORRESPONDENCE: ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                             Method and Products For the Synthesis of Oligosaccharide Structures on Glycoproteins, Glycolipids, or as Free Molecules, and For the Isolation of Cloned Genetic Sequences That Determine These Structur
                                      TTTAAGCCAGAGCCAGCCTTCCTACCCGAATGGGTGGGCATCCCTGCCGATCTGTCCCCA 1050
   992 GGCGGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGATC 1051
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                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                           ALDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Suite 400 CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00899
FILING DATE: 19910214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 405; DB 5; I Pred. No. 2.1e-108;
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ATTORNEY/AGENT INFORMATION:
NAME: LAVALIBYE Ph.D., Jean-Paul
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
TELECOMMUNICATION INFORMATION:
TELEFAX: (703)521-5940
TELEFAX: (703)466-2347
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                               Sequence 10, Application PC/TUS9100899 GENERAL INFORMATION:
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577; Conservative
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TISSUE TYPE: Blood
PCT-US91-00899-10
                                                                                                                                                                                                                                                              APPLICANT: LOWE, JOH
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                                                                                                          CTC 1053
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Best Local
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APPLICANT: Sandrin, Mauro S.
APPLICANT: Fodor, William L.
APPLICANT: Stother, Wissell P.
APPLICANT: Squinto, Stephen P.
APPLICANT: McKenzle, Ian R. C.
TITLE OF INVENTION: Methods for Reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: ALX-144.1PCT TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS 6.2
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION: HUMAN H-transferase HYPOTHETICAL: NO
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APPLICATION NUMBER: 08/278,28;
FILING DATE: July 21, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 750
COMPUTER: Dell 486/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/260
FILING DATE: June 15, 1994
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TELEFAX: (203) 254-1101
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1951 Burr Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1174 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
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ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Larsen, R.D.
AUTHORS: Ernst, L.K.
AUTHORS: Nair, R.P.
AUTHORS: Lowe, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Connecticut
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CITY: Fairfield
STATE: Connection
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1136;
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Pred. No. 2.2e-108;
0; Mismatches 260; Indels
         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATIG SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,800A
FLING DATE: 28-FEB-1995
CLASSIFICATION: 435
TELECOMMUNICATION: 10FRMATION:
TELECOMMUNICATION: 7703 413-220
                                                                                                                                                                                                                                                                                                                                                                                                                     35.2%;
                                                                                                                                                                                                                                                   TENGTH: 1136 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 68.4 Matches 577; Conservative
COMPUTER READABLE FORM:
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39..1133
                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                  ;
US-08-395-800A-9
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FEATURE:
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1053 TITAAGCCGAGGCGCCTTCCIGCCCGAGTGGGGGATTAATGCAGACTIGTCTCCA 1112
                                                                                                                                                   991 ITTAAGCCAGAGGCAGCCTTCCTACCCGAATGGGTGGGCATCCCTGCCGATCTGTCCCA 1050
931 GGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGTTCCTCAAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rejection of Xenografts
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us-10-040-863-7.rni

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Score 405; DB 1; I
Pred. No. 2.3e-108;
0; Mismatches 260;
                                                                                                                                                                                             TITLE OF INVENTION: GDP-L-FUCOSE: BETA-I
TITLE OF INVENTION: 2-ALPHA-L-FUCOSYLTRA
TITLE OF INVENTION: SAME, METHOD FOR PRO
TITLE OF INVENTION: GENOTYPING A PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US/08/395,800A
28-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                    Sequence 5, Application US/08395800A
Patent No. 5807732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-300
TELEFAX: (703) 413-220
TELEFAX: 240855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                    APPLICANT: ROUQUIER, SYLVIE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.2%;
Local Similarity 68.4%;
nes 577; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 1199 base pairs
nucleic acid
EDNESS: double
                                                                                                                             LOWE, JOHN B
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                                                                                                             GENERAL INFORMATION: APPLICANT: LOWE,
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US-08-395-800A-5
                                                        RESULT 12
US-08-395-800A-5
                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                    Length 1174;
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                                                                                                                                                                  Score 405; DB 5; L
Pred. No. 2.3e-108;
0; Mismatches 260;
Molecular cloning, sequence, and expression of a human GDP-L-fucose:
-p-galactoside 2-alpha-L-fucosyltransferase cDNA that can form the H blood group antigen.
L: Proceedings of the National L: Academy of Sciences, USA
                                                                                                                                                                  35.2%;
68.4%;
                                                                                                                                                                               Local Similarity 68.4 nes 577; Conservative
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SEP-1990
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Best Local Si
Matches 577;
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GDP-L-FUCOSE: BETA-D-GALACTOSIDE
2-ALPHA-L-FUCOSYLTRANSFERASES, DNA SEQUENCES ENCODING
SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
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                                                                                                                                  SSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
:: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
ARLINGTON
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1529 TITAAGCCGGAGGCGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA 1588
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                                                                                                                                                                                         Length 2268;
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Pred. No. 3.1e-108;
0; Mismatches 260;
DIAMOND=1A
      TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2268 base pairs
                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                   35.2%;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                 Best_Local Similarity 68.4
Matches 577; Conservative
                                                                                               TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                             linear
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US-08-675-773B-4
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                     GTGCGCCGAGGGGACTATGTGCATGTCCTAATGTGTGGAAGGGCGTGGTGGCTGAC
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APPLICANT: BYRNE, GUERARD W
APPLICANT: STARMA, AJAY
TITLE OF INVENTION: METHOD OF PRODUCING TRANSGENIC ANIMALS
TITLE OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWNY ANT
STREES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
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419 SEVENTH STREET, N.W., SUITE 300
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APPLICATION NUMBER: US/08/675,773B
FILING DAIE: 03-JUL-1996
CLASSIFICATION: 800
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28.(
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CTC 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LOGAN, JOHN S
APPLICANT: BYRNE, GUERARD W
APPLICANT: SHARMA, AJAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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US-08-675-773B-3
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Pred. No. 3.7e-108;
0; Mismatches 260; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,411
                                                                                                                                                                                                                                                         3: Patrea L. Pabst
1100 Peachtree Street, Suite 2800
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                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Falk, Per
APPLICANT: Gradon, Jeffrey I.
APPLICANT: Gordon, Jeffrey I.
TILLE OF INVENTION: Animal Model for TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: WU10
TELECOMMUNICATION INFORMATION:
TELEFAN: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3373 base pairs
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                                                                                                               Sequence 2, Application US/08273411 Patent No. 5625124
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NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
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ilarity 68.4%;
Conservative
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LOCATION: 104..1201
OTHER INFORMATION: /rote-
PUBLICATION INFORMATION:
AUTHORS: Larsen, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: double
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CLASSIFICATION: 435
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US-08-273-411-2
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Pred. No. 3.9e-108;
0; Mismatches 260; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,773B
FILING DATE: 03-UL-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, 179ER P.
                                                                                                                                    DIAMOND=1A
                                                                                                                     RECISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: DIAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3791 base pairs
                                                                                                                                                                                                                                                                , MOLECULE TYPE: DNA (genomic) US-08-675-7738-3
                                                                                                                                                                                                                                                                                                       Query Match 35.2%;
Best Local Similarity 68.4%;
Matches 577; Conservative
                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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QY 992 TTTAAGCCAGAGCAGCTTCCTGCCAATGGTGGCAGCTCTGCCCCA 1050

QY 1051 TTTAAGCCGAGCGCCTTCCTGCCGAGTGGGTGGCATTAATGCAGACTTGTCTCCCA 3132

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GENERAL INFORMATION:

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APPLICANT: Eric H. Holmes et al.
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TITLE OF INVENTION: GAL-SPECIFIC ALPHA1-2 FUCOSYI
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/10/040,863
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/298,886
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VET. 2.0
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              TACCACCACCTGCGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAG
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                                                    GCATCCATGCACACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGG
                                                                    TACCGCCACATICCGGGACACITIGICCGCTICACGGGATACCCGTGCTCCTGGACCTIC
                                                                                                                                                                           APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLICSIDE
TITLE OF INVENTION: GAI-SPECIFIC ALPHAI-2 FUCOSYLITRANSFERASE AND US
TITLE OF INVENTION: THEREOF
FILE REPRENCE: 8511-029
CURRENT APPLICATION NUCLEIC US/10/040,863
CURRENT FILING DATE: 2001-11-01
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Patent No. US20020137165A1
GENERAL INFORMATION:
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APPLICANT: Eric H. Holmes et al.

APPLICANT: Eric H. Holmes et al.

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: NGLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE

TITLE OF INVENTION: GAL-SPECIFIC ALPHAI-2 FUCGSYLTRANSFERASE AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/999,672

CURRENT FILING DATE: 1099-101-10-31

PRIOR FILING DATE: 1099-104-26

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATENTIN VET. 2.0
                                                                                                TCGCCAGCCAAGGACTTTCGCGCTGCTCACCCAGTGCAACCACATCATGACTATTGGG
                                          CGGGAGAACATTAATGCTTCCCGAGGAGACGTGTGTTCGCGGGCAATGGTATTGAGGGG
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Best Local Similarity 100.
Matches 1068; Conservative
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; LOCATION: (1)..(1062)
US-09-999-672-9
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US-09-999-672-9
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              1042 CTGTCCCCACTCCTTAAGGCATTAACACCAGCCTGTCCTCGGTCCCACTTCCACGTCAAG
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                                                                                                                                                                                                                                                                    Sequence 1, Application US/09051034A
| Patent No. US2001005584A1
| GRNERAL INFORMATION
| APPLICANT: MCKENZIE, IAN FARQUHAR CAMPBELL
| APPLICANT: SANDRIN, MAUNO SERGIO
| TITLE OF INVENTION: GLYCOSYLTRANSFERASE
| FILE REPRENDE: 30562.6U5W0
| CURRENT APPLICATION NUMBER: US/09/051,034A
| CURRENT FILING DATE: 1998-03-31
| PRIOR APPLICATION NUMBER: 60/024,279
| PRIOR FILING DATE: 1996-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 1043;
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US-09-051-034A-1
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100.0%; Pred. No. 0;
ive 0; Mismatches
PRIOR APPLICATION NUMBER: 09/298,886 PRIOR FILING DATE: 1999-04-23
                                                                                     TYPE: DNA
ORGANISM: Rattus norvegicus
                         NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                                                 Best Local Similarity 100.
Matches 1068; Conservative
                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (1)..(1062)
US-10-040-863-9
                                                                      LENGTH: 1068
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                                                                                                                                                                                                                                  53.3%; Score 612.6; DB 1073.8%; Pred. No. 1.5e-185;
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFWWARE: PATCHIN VETSION 3.0
SEQ ID NO 45
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                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
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Matches 808; Conserv
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Fatent No. US20020115057al
GENERAL INFORMATION:
APPLICAMY: Young, Paul
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/69/954,456
CURRENT PILING DATE: 2001-09-18
FRICH REPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
FRICH REPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-25
FRICH REPLICATION NUMBER: US/60/234,923
FRICH REPLICATION NUMBER: US/60/234,923
FRICH REPLICATION NUMBER: US/60/235,134
FRICH REPLICATION NUMBER: US/60/235,134
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| 180 CACTATATITCACGITCAGCAGCGGTAGCGAAGATTCAAGCCATGTGGGAGTTACCGGT 235  129 ACCGATGACGATCCAATGTCCTCGGAAACACACAGAAGCCCAGGATGCGACGG 188 | 309 TGCGTTCATCCCCGCATCCATGCACAGCGCCCATCTTCAGGATCAGCCTCC 368   | 10   | 669 GTGGAAGGGCTGGTGACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGC 728   | 987 GATCTGGGCGGGATACCTCAGGGGGGAGACCATCTACCTGGCCAATTACACCCTCCC 1046 969 GGATTCTCCGTTCCTCAAGTCTTTAAGCCAGAGGCAGCCTTCCTACCCGAATGGGTGGG   |
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|  | 1029 CATCCTGCCGATCTGTCCCTTAAGGCATTAACACCAGCTGTCCTCGGTCCCA 108 | US-09-954-456-1621  ; Sequence 1621, Application US/09954456 ; Patent No. US20020115057A1 ; GENERAL INFORMATION:     APPLICANT: Young, Paul     TITLE OF INVENTION: Sets ; FILE OF INVENTION: Sets ; FILE REFERENCE: 689200-76 ; CURRENT FILING DATE: 2001-09-18 ; PRIOR PAPLICATION NUMBER: US/09/954,456 ; CURRENT FILING DATE: 2001-09-18 ; PRIOR APPLICATION NUMBER: US/60/233,617 ; PRIOR FILING DATE: 1000-09-18 ; PRIOR APPLICATION NUMBER: US/60/234,052 | ELLING DATE: 2000-09-20 APPLICATION NUMBER: US/60/234,92 FILING DATE: 2000-09-25 APPLICATION NUMBER: US/60/235,13 FILING DATE: 2000-09-25 APPLICATION NUMBER: US/60/235,63 FILING DATE: 2000-09-26 APPLICATION NUMBER: US/60/235,63 APPLICATION NUMBER: US/60/235,63 APPLICATION NUMBER: US/60/235,72 FILING DATE: 2000-09-27 APPLICATION NUMBER: US/60/235,72 FILING DATE: 2000-09-27 APPLICATION NUMBER: US/60/235,73 FILING DATE: 2000-09-27 APPLICATION NUMBER: US/60/235,84 FILING DATE: 2000-09-27 APPLICATION NUMBER: US/60/235,84 FILING DATE: 2000-09-27 APPLICATION NUMBER: US/60/235,84 FILING DATE: 2000-09-27 APPLICATION NUMBER: US/60/235,86 FILING DATE: 2000-09-27 FILING DATE: 2000-09-27 FILING DATE: 2000-09-27 | ; SOFTWARE: Patentin version 3.0; SOFTWARE: Patentin version 3.0; SEQ ID NO 1621 ; EDOUTH: 3088 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-954-456-1621 Guery Match  Est Local Similarity 73.8%; Score 612.6; DB 10; Length 3088; Best Local Similarity 73.8%; Pred. No. 1.5e-185; Matches 808; Conservative 0; Mismatches 254; Indels 33; Gaps 1;  QY 9 CGCCAGGTTCTTTCTTTCTTTCTTTCTTTCGTGACTTCGTGACTTC 68 |

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1047 CGACTCCCCTTTCCTCAAATCTTTAAGCCAGAGCAGCCTTCCTGCCGGAGTGGACAGG 1106
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       729 ACGCIATTCAICTCCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAA
                                                                                CATIAATGCTTCCCGAGGAGGTGGTGTTCGCGGGCAATGGTATTGAGGGGTCGCCAGC
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APPLICANT: MCKENZIE, IAN FARQUHAR CAMPBELL
APPLICANT: ACKENZIE, IAN FARQUHAR CAMPBELL
APPLICANT: ACKENZIE, IAN FARQUHAR CAMPBELL
TITLE OF INVENTION: MAURO SERGIO
TITLE OF INVENTION: GLYCOSLITRANSFERASE
FILE REFERRENCE: 30562.6USWO
CURRENT APPLICATION NUMBER: US/09/051,034A
CURRENT FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: PCT/AU97/00492
PRIOR PLING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: 60/024,279
PRIOR PLING DATE: 1996-08-21
PRIOR PELING DATE: 1996-08-21
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Pred. No. 2.6e-125;
0; Mismatches 252;
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; LOCATION: (1)..(1098)
US-09-051-034A-3
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US-09-051-034A-3
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Best Local S:
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Sequence 234, Application US/09969347

Battent No. US20020115085A1

GENERAL INFORMATION:

APPLICANT: Edner, Reinhard

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturities of INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturities of INVENTION: Sets

FILE REPERENCE: 689290-69

CURRENT APPLICATION NUMBER: US/09/969,347

CURRENT APPLICATION NUMBER: US/60/237,598

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER: OF SEQ ID NOS: 318
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Pred. No. 1.5e-185;
0; Mismatches 254; Indels 33;
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LENGIH: 3088
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TILLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
TITLE OF INVENTION: RESISTANT TO FIB E. COLI ASSOCIATED DISEASES
TITLE OF INVENTION: RESISTANT TO FIB E. COLI ASSOCIATED DISEASES
CURRENT APPLICATION NUMBER: US/09/844,268
CURRENT APPLICATION NUMBER: 09/443,766
PRIOR APPLICATION NUMBER: 09/443,766
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 12
LENGIH: 1269
TYPE: DNA
TYPE: DNA
ONNAMENTED PATENTINE PATENTIN
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                                                GCTCCTTGGCGGGGGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG
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APPLICANT: BOSWORTH, BRAD
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                                                                                                                                            GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCCGAGGTAGACAGGCAC
                                                                                                                                                                                                                                                                                            ATCCCATGGCAGAATTACCATCTCAACGACTGGATGGAGGAGCGTTACCGCCACATTCCG
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Length 1269;
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DB 10;
                                  0; Mismatches 252;
Score 423.8; DB 10
Pred. No. 2.8e-125;
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36.9%;
                                  Conservative
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                 Similarity
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Query Match 35.2
Best Local Similarity 68.4
Matches 577; Conservative
                                                                                        CTCCTTAAG 1059
                                                                                                              1083 CTCCAGATG 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (164)..(1201);
CTHER INFORMATION:
US-10-105-963-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
                                                                                                                                                                   US-10-105-963-9
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APPLICANT: VOGELI, PETER
TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
FILLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
FILLE PEPERBUCE: 21419/90368
CURRENT APPLICATION NUMBER: US/09/844,705
PRIOR PELIOR DATE: 1909-1443,766
PRIOR FILLING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VOS: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         517 CCAGAGAICCIGAAGGAGITCACCCTGCAIGACCACGIGCGGGAGGAGGCCCAGGCCIIC 576
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                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                     36.9%; Score 423.8; DB 10;
69.6%; Pred. No. 2.8e-125;
iive 0; Mismatches 252;
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (9)..(1103)
US-09-844-705-12
                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                           TYPE: DNA ORGANISM: Porcine
                                                                                                                                 SEQ ID NO 12
LENGTH: 1269
                                                                                                                                                                                                                                                                              591;
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Sequence 9, Application US/10105963
Fublication No. US20030068818A1
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Clark, A. John
APPLICANT: Clark, A. John
TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
TITLE OF INVENTION: Recombination
TITLE OF INVENTION: Recombination
TITLE OF INVENTION: Recombination
FILE REFRENCE: 731/002
CURRENT FILING DATE: 2002-03-21
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin version 3.1
SECOND SEQ ID NOS: 40
963 GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGGTTCCTGAAGATC 1022
                                                                                                    1023 TTTAAACCCAGGGTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCC 1982
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                                                          991 TITAAGCCAGAGCAGCCTTCCTACCCGAATGGGTGGGCATCCCTGCCGAICTGTCCCCA
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                                                                                                                                                               Length 8174;
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                                                                                                                                                                                                  0; Mismatches 260;
                                                                                                                                                                 Score 405; DB 10;
Pred. No. 6.2e-119;
                                                                                                                                                               Score 405;
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                                                                                                            SEQUENCE DESCRIPTION: SEQ ID
                                                        TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
       LENGTH: 8174 base pairs
                       TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                               35.2%;
                                                                                                                                                                                                    Conservative
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577;
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APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
                                                                                                                                                                                                                                                                                 TTTAAGCCAGAGGCAGCCTTCCTACCCGAATGGGTGGGCATCCCTGCCGATCTGTCCCCA 1050
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CGGGGTTACCTGGAAAAGGCCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCTTC
                                                                                      AGCGCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGGTTTTC
                                                                                                                       GTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCCCGAGGAGAC
                                                                                                                                                                                                                                                                                                                                                                      GGCGGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGATC
                                                                                                                                                                                             GIGGIGITCGCGGCAATGGTATTGAGGGTCGCCAGCCAAGGACTTCGCGCTGCTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRIN APPLICATION DATA:
APPLICATION NUMBER: US/09/863,475A
FILING DATE: 24-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lavalleye, Jean-Paul M. P.
REGIESTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

**PAPLICATION NUMBER: 07/914,281

**FLING DATE: 20-JUL-1992

ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09863475A Patent No. US20020102688A1 GENERAL INFORMATION: APPLICANT: LOWE, JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 248855 OPAT UR INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS;
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STATE: Virginia
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US-09-863-475A-5
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APPLICANT: Eric H. Holmes et al.
APPLICANT: Eric H. Holmes et al.
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: UGCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: UGAL-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/10/040,863
CURRENT APPLICATION NUMBER: US/298,886
PRIOR APPLICATION NUMBER: 09/298,886
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                      GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Eric H. Holmes et al.

AITLE OF INVENTION: HOLMES CIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GM1-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT FILING DATE: 2001-10-31
PRIOR PAPLICATION NUMBER: US/09/298,886
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29
LENGTH: 100
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6.3%; Score 72.8; DB 12; Length 100;
Best Local Similarity 83.0%; Pred. No. 2.4e-13;
Matches 83; Conservative 0; Mismatches 17; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 72.8; DB 10; Length 100;
Pred. No. 2.4e-13;
0; Mismatches 17; Indels 0
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US-10-040-863-29
Sequence 29, Application US/10040863
Patent No. US20020137165A1
                          Sequence 29, Application US/09999672
Patent No. US20020127655A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Oryctolagus cuniculus
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; ORGANISM: Oryctolagus cuniculus
US-09-999-672-29
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Best Local Similarity 83.0%;
Matches 83; Conservative (
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SEQ ID NO 29
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827 ATGGTATTGAGGGGTCGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCACAA 886 887 ICAIGACIATIGGGACCITIGGGATITIGGGCIGCCIACCI 926 Search completed: May 26, 2003, 15:19:53 Job time: 178.211 secs

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BM764788 AL046138 BM764751 BF710517 BB849545 BH274506

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BM773356 BB8489719 BB8489719 BB848710 BB756417 BB756417 BB756417 BB756910 BB756910 BB756910 BB7091033 BB7091033

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May 26, 2003, 10:09:53; Search time 1886.5 Seconds (without alignments) 9864.119 Million cell updates/sec
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BQ920588 /
BE266792 (
BM744084 I
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BM781532 I
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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BQ920588
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                                       nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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ALIGNMENTS

AI606683 AA108903

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BE667589 BE0109528 BE01027 AW917919 AW917919 BI350052 BH342943 AUT00082 AL709188 BM742943 BM742943 BM742943 BM742943 BM742943 BM742944

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|-----------|----------------------|---|
|           | RESULT 1<br>BB624949 |   |
|           | LOCUS                | BB624949 656 bp mRNA linear EST 31-AUG-2001                               |
|           | DEFINITION           | BB624949 RIKEN full-length enriched, adult male colon Mus musculus        |
|           |                      | cDNA clone 9030420L11 5', mRNA sequence.                                  |
|           | ACCESSION            | BB624949  |
|           | VERSION              | BB624949.1 GI:15398432  |
|           | KEYWORDS             | BST.  |
|           | SOURCE               | house mouse.  |
|           | ORGANISM             | Mus musculus  |
|           |                      | Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,         |
|           |                      | Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.        |
|           | REFERENCE            | 1 (bases 1 to 656)  |
|           | AUTHORS              | Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanaqaki, T., Hara, A. |
| or or     |                      | , Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda |
| inted,    |                      | , M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,        |
|           |                      | Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki       |
|           |                      | ,D., Shibata,K., Shinaqawa,A., Shiraki,T., Soqabe,Y., Suzuki,H.,          |
|           |                      | Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,  |
| =         |                      | Muramatsu, M. and Hayashizaki, Y.   |
|           | TITLE                | RIKEN Mouse ESTs (Arakawa,T., et al. 2001)                                |
| ċ         | JOURNAL              | Unpublished (2001)  |
|           | COMMENT              | Contact: Yoshihide Hayashizaki  |
| BB624949  |                      | Laboratory for Genome Exploration Research Group, RIKEN Genomic           |
| AGENCOURT |                      | Sciences Center(GSC), Yokohama Institute '.                               |
| 601190486 |                      | The Institute of Physical and Chemical Research (RIKEN)                   |
| K-EST0017 |                      | 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaqawa 230-0045, Japan        |
| K-EST0046 |                      | Tel: 81-45-503-9222   |
| K-EST0058 |                      | Fax: 81-45-503-9216   |

360 453 420 513 480 573 540

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/dlone="ImAGE:6497629"
/clone=lib="NMIH_MGC_101"
/tissue_type="epidermoid carcinoma, cell line"
/tissue_type="epidermoid carcinoma, cell line"
/tab_host="billoB (phage-resistant)"
/note="Organ: lung: Vector: pOTB): Site_1: ECORI; Site_2:
XhoI; CDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the [20]owing 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (Uhiversity of California, Borkeley) using 2AP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ920588 1133 bp mRNA linear EST 20-AUG-2002 AGENCOURT_10016100 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6497629 5', mRNA sequence.
              CGGGACAGCGAGCATGGAATGGAGAGCTGCGGGGCATGTTCACGATCAATTCCATT
                                                                                                        -------CAGCAGAGTGCCAAGCTGCAGGGCATATTCACGATCAATTCCATC
                                                                                                                                                    GGCCGGCTGGGGAACCAGATGGGCGAATACGCCACACTCTTTGCACTGGCCAGGATGAAC
                                                                                                                                                                            GGACGGCTTGCGTTCATCCCGCATCCATGCACACGCTCTAGCGCCCCATCTTCAGGATC
                                                                                                                                                                                                                                                                                         394 GGTCGGCTTGCCTTCATCCTGAATCCATGCACAACGCTCTAGCGCCCATCTTCAGGATC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homc.
1 (bases 1 to 113)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 440.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                                                                                                                                                                                                                                                          RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Evkunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
Email: genome-reségsc.riken.go.jp,
URL:http://genome.go.gr.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.P., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GTGACTTCCACCATCATCCACCTCCAGCGAATAGTGAAGCTCCAACCCCTGTCAGAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 410; DB 10; Length 656;
Pred. No. 1.7e-102;
0; Mismatches 57; Indels 21; Gaps
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="colon"
/dev_stage="adult"
/lab_host="DH10B"
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DEFINITION

ACCESSION VERSION KEYWORDS

RESULT 3 BE266792

AUTHORS TITLE

REFERENCE

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/clone_lib="NIH_MGC_7"
/clone_lib="NIH_MGC_7"
/tissue_type="Small cell carcinoma"
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/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5;
adaptor: GGCAGGGG(G). Size-selected >500Pp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using 2AP-cDNA synthesis kit
(Stratagen) and Superscript II RT (Life Technologies)."
45 a 233 c 203 g 132 t
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 714)
1 (hases 1 to 714)
1 Nat-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (Unpublished (1999)
                                                                 Length 1133;
                                                                                                 1:
                                                                                                 Indels
                                                                 DB 14;
                                                                                                 Mismatches 114;
                                                             Score 398.6; DB 1
Pred. No. 3.3e-99;
                  221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: egapbs r@mail.inh.gov ... Plate: LLCM213 row: 1 column: 22 High quality sequence stop: 639.
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Library."
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                                                             34.7%;
80.6%;
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                                                                                             478; Conservative
                332
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us-10-040-863-7.rst

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                                                                                                                                                                Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, M.Y., Chong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and 21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACCATCATCCACCTCCAGCAGCGAATAGTGAAGCTCCAACCCCTGTCAGAGAAGTT 128
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 ACCGATGACGACTCAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGACGGGACAG
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                                                                                                                                                                                                                                                                                                                                                      52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-866-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 24.6%; Score 283; DB 14; Length 596; al Similarity 71.7%; Pred. No. 2.5e-67; 401; Conservative 0; Mismatches 125; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 GCAGATACCAGTGCTAGCCTCAACATCAAAGGCACTGGGACCCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Lymphoblast-like"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/clone="838NU16-14-A06"
/clone=_ilb="838NU16"
/sex="F"
                                                                                                                                                                                                                                                                                                                                                                                                                             Email: yongsungemail.kribb.re.kr
Plate: 14 row: A column: 06
High quality sequence stop: 596.
Location/Qualifiers
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BM744084.1 GI:19065413
mRNA seguence.
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                                                                                       human.
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/note="Organ: Stomach; Vector: pT218RP1; Site_1: EcoRI: Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coll DNA ligase after digestion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM764661 S3SNU16s1 Homo sapiens cDNA clone S3SNU16s1-7-H02 5',
                                                                                                                                                                                                                     428
                                              278 GGGGAACCAGATGGGGGAGTACGCCACACTGTACGCCCTGGCCAAGATGAACGGGCGGCC 337
                                                                                                                                                              397
                                                                                                                                                                                                                                                  429 GATGGAGGAGCGTTACCGCCACATICCGGGACACTITGTGCGCTTCACGGGATACCCGIG 488
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R. Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
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                                                                                                            309 TGCGTTCATCCCGGCATCCATGCACACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCC
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuscong-gu, Daejeon 305-333, South Korea
Fal: +82-42-860-4409
Fax: +82-42-860-4409
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/cell_type="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="Top(0F'"
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Unpublished (2002)
Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/sex="F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: yongsung@mail.kribb.re.kr
Plate: 7 row: H column: 02
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BM764661
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BM781532.1 GI:19129764

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VERSION
KEYWORDS
ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant CDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of blottinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded CDNAs prepared from original
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                                                                                                                                                                                                                                                                                                                                       liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with electroporation method."
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Pred. No. 3.16
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71.28;
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Matches 394; Conservative
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BM781532 591 bp mRNA linear EST 05-MAR-2002 K-EST0058109 53SNU16s1 Homo sapiens cDNA clone S3SNU16s1-19-B07 5',

mRNA sequence. BM781532

DEFINITION

RESULT 6 BM781532

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/note="Organ: Stomach; Vector: pTz18RP1; Site_1: ECORI; Site_2: Not1: The poly (A)+ RNA was dephosphozylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of T4 RNA ligase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60Mt. The CDNA vector was circularized with E. coli DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained CDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched CDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted constructed by transformation of the commandance of the constructed by transformation of the constructed by transformation of the constructed.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 591)
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21C Frontier Korean EST Project 2001
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/cell_type="Tymphoblast-like"
/cell_line="SNU-16"
/cell_host="Top10F'"
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and 21C Frontier Korean EST Project 2001
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                        /note="Organ: Stomach; Vector: pTZ18RP1; Site_1: ECORI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of T4 RNA ligase and the first strand CDNA was synthesized from Oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 272.4; DB 14;
Pred. No. 2.1e-64;
0; Mismatches 126; I
lab_host="Top10F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.7%;
71.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 71.1
Matches 391; Conservative
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E. I. (bases I to 592).

S. Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R., Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and Kim, Y. S.

I. Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eceun-dong Yusecong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4410

Email: yongsung@mail. Kribb.re.kr

Plate: 5 row: H column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organis Stomach; Vector: pTz18Rp1; Site_1: ECORI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of T4 RNA ligase and the first strand CDNA was synthesized from Oilgo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coll DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayèma-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coll ToplOF' by electroporation method. The CDNA libraries constructed by this method are
                                                                                                                                                                                                                                                            975 TCCGITCCTCAAAGTCITTAAGCCAGAGCCAGCCTTCCTACCCGAATGGGTGGGCATCCC 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM764751 592 bp mRNA linear EST 04-MAR-2002
K-EST0046310 S3SNU16S1 Homo sapiens CDNA clone S3SNU16s1-5-H66 5',
                        298
                                                                                                                                                                                           GGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTACACCTTCCGGATTC 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                       CTTCGCGCTGCTCACCCAGTGCAACCACCATCATGACTATTGGGACCTTTGGGATTTG
/cell_type="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="Topl0F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="S3SNU16s1-5-H06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Ascites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="S3SNU16s1"
/sex="F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: 5 row: H column: 06
High quality sequence stop: 5
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BM764751
BM764751.1 GI:19094366
                                                                                                                                                                                                                                                                                                                                                       1035 TGCCGATCT 1043
                                                                                                                                                                                                                                                                                                                                                                                                    479 GGCIGACCT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM764751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                915
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM764751
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                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                 DKFZp434P0672_r1 434 (synonym: htes3) Homo sapiens CDNA clone
DKFZp434P0672_r1 434 (synonym: htes3) Homo sapiens CDNA clone
AL046138
AL046138.2 GI:5936190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 CCGCCTCCCGGTCTTTGTGTCACCAGCGATGACATGGCCTGGTGCCGGGAGAGCATCAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   795 TGCTTCCCGAGGAGGACGTGTTCGCGGGCAATGGTAITGAGGGGGTCGCCAGCCAAGGA 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09
                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department Lehrach
Max-Planck Institute for Molecular Genetics
Ihnestrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131628
Fax: +49-30-84131128
Email: poustka@mping-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Emails s. Wiemann(dKfz- heidelberg.de;
Sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germanny) within the CDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No s1 sequence available.
This clone (DKFZp434P0672) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 764)
Poustka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (boustka, et al.)
Unpublished (1999)
On Jul 9, 1999 this sequence version replaced gi:5434225.
Contact: Poustka A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   615 TTTTGTGGGTGTCCATGTGCGCCGAGGGACTATGTGCATGTCATGCCTAATGTGTGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCGTGGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        735 TTCATCTCCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGACATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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248 g 157 t 3 others
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Pred. No. 3.6e-64;
0; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="434 (synonym: htes3)"
/fssue_vype="testis"
/dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="DKFZp434P0672"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector:
234 c 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 360; Conservative
CCACGTGCGG 558
                                       578 CCACGIGGG 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                 ACCESSION
                                                                                                               RESULT 8
AL046138
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δŽ Dρ ŏ g δŽ g  $\delta$ g δŏ facilitate gene

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/organism="Sus scrofa"
/strain="crossbreed"
/db_ref="texon:982"
/db_ref="texon:982"
/clone="Inb="MI-P-AXI-nre-a-12-0-UI"
/clone="Inb="MI-P-AXI"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-AXI
library is normalized library derived from the MI-P-AXI
library, ultimately derived from placenta tissue. For a
detailed description of the library from which this clone
was derived, please visit our web site at
http://pigest.genome.lastate.edu/. The procedure used to
create this library has been previously described (Bonaldo
, Lennon and Scares, Genome Research 6: 791-806, 1996)
                                                                                                                                                                                                                                                                                                            Email: cxtugglegiastate.edu

The sequence contained an oligo-dr track that was present in the oligonucleoride that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to verify it as a clone from the normalized placenta library CDNA Library Preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1011 CCTACCCGAATGGGTGGGCATCCCTGCCGATCTGTCCCACTCCTTAAGGCATTAACACC 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       711 CCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCTTCGTGGTTACAAGCAACGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCCAACTACACCTTCCGGATTCTCCGTTCCTCAAAGTCTTTAAGCCAGAGGCAGCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    771 GGCCTGGTGCCGGGAGAACATTAATGCTTCCCGAGGAGACGTGGTGTTCGCGGGCAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     831 TATTGAGGGGTCGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACTATTGGGACCTTTGGGATTTGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTT
                                                                                                                                                                                        Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Far: 5152944252
Fax: 5152942401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 521;
  Butheria; Cetartiodactyla; Suina; Suidae;
1 to 521)
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                                                                       Normalization and subtraction: two approaches
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Pred. No. 2.2e-57;
                                                Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research Genetics (www.resgen.com)
                                                                                                                        Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAG_TISSUE=placenta
TAG_SEQ=ATTGG"
119 c 170 q
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1. .521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.5%; 79.1%;
                                                                                                                                                                      Contact: Tuggle CK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 21.5
Best Local Similarity 79.1
Matches 306; Conservative
  Mammalia; Euthe
1 (bases 1 to
Bonaldo,M.F., I
                                                                                                    discovery
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                                                                                                                                             MEDLINE
COMMENT
                         REFERENCE
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                                                                       TITLE
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            sequencing about 2.000 -3.7000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5 primer and N(dT)14 as 3 primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avoidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with electroporation method."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTTCAGATGCCTTTCTCCTTTCCCATGGCCCACTTCATCCTCTTTGTCTTTACGGTTTC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACCATCATCCACCTCCAGCAGCGAATAGTGAAGCTCCAACCCCTGTCAGAGAAGGAATT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 ACCGATGACGACTCAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGACGGGACAG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTGTTACACAGCGACACGGCCAAAAAGATCCCAIGGCAGAATTACCATCTCAACGACTG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGGAGGAGCGTTACCGCCACATTCC-GGGACACTTTGTGCGCTTCACGGGATACCCGT 487
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 TGCGTTCATCCCCGCATCCATGCACAACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
full-length enriched cDNA library. After analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 592;
                                                                                                                                                                                                                                                                                                                                                                                              Score 265.4; DB 14; Pred. No. 1.9e-62; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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201 c 155 g 1
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71.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 395; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA 721: 301 838 0200
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                                                                                                                                                                                                                                                                                                                                                                                                                  61 GTGACTTCCACCATCATCCACCTCCAGCAGAGATAGTGAAGCTCCAACCCCTGTCAGAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 CGGGACAGCGAGCAGCATGGGAATGGAGGGGGGGGGGGTTCCACGATCAATTCCATT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AAGGAATTACCGATGACGACTCAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGA 180
   sex-mnixed), (tissue_type=hippocampus, dev_stage=adult,
sex=mnle), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed),
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 GGTCGGCTTGCCTTCATCCCTGAATCCATGCACGAACGCTCTAGCGCCCATCTTCAGGATC
                                                                                                                                                                                                                                                                                                                 Gaps
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Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Conher_GSS: CH230-23110.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                              Length 440;
                                                                                                                                                                                                                                                                                                              40; Indels
                                                                                                                                                                                                                                              Score 243; DB 10;
Pred. No. 2.5e-56;
0; Mismatches 40;
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83.5%;
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308; Conservative
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Rattus norvegicus
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Hayatsu, N., Hiramoto, K., Hiraoka, T., Hrozane, T., Imotani, K., Ishii
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hrozane, T., Tuo, M., Matsuyama, T.,
Nakamura, M., Nakhi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Salto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shidata, K., Shinaqawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Taqawa, A., Takahashi, F., Ishkau-Akhira, S., Tanaka, T., Tomaru, A., Takahashi, F., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itch,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                       BB849545 RIKEN full-length enriched, adult inner ear Mus musculus cDNA clone F930101E05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-resigns.riken.go.jp,
URL:http://genome.go.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashiaaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
penes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-922
Fax: 81-45-503-9216
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Y, and Hayashizaki'y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN integrated sequence analysis (RISA) system--384-format
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/note="pooled tissues; (tissue_type=cerebellum,
dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
                                                                                                       1097
                                                                                                                                                                       162 GGCTGGTCCTCGGCTCCCCATTCTTCT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="inner ear"
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/db_xref="taxon:10090"
/clone="F930101E05"
                                                                                                       1071 AGCCTGTCCTCGGTCCCACTTCCACCT
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K-EST0057795 S3SNU16s1 Homo sapiens cDNA clone S3SNU16s1-17-H05 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 522)
Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R., Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and
                                                                                                                                                                                                                                                                                                                                                                                                  ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                   598 GGGAGCCAGCCGAGTACTTTGTGGGTGTCCATGTGCGCCGAGGGGACTATGTGCATGTC 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 GGCATCCGTCCTCGTACCTAIGTGGGTGTTCACGTGGGTCGTCGTGGAGACTCTTTGGAGGTG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGCCTAATGTGTGGAAGGCGTGGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGAT 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 ATGCCTAACCGCTGGAAGGGAGTGGTGGGTGACCGAGCTTACCTCCAGAAAGCCATTGAC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             718 ATGIICCGGGCACGCIATICATCTCCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGG 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 TGGTTCCGGGCCCGGCACAAAGACCCCATCTTTGTGGTCACCAGCAATGGCATGAGATGG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       778 IGCOGGGAGAACATTAATGCTTCCCGAGGAGACGTGGTGTTCGCGGGCAATGGTATTGAG 837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGACCITIGGGAITIGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAAC 957
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                                                                                                                                                                                                                 /cell_type="Brain"
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CHORI-230 Rat [BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"
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Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                                                                                                                       20.2%; Score 232.2; DB 17; Length 74.8%; Pred. No. 2.5e-53; ive 0; Mismatches 98; Indels
                                                                                                                                   /db_xref="taxon:10116"
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                                                                                              /organism="Rattus norvegicus"
//strain="BN/SsNHsd/MCW"
                                                                                                                                                                                                                                                                                               108 t
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21C Frontier Korean EST Project 2001
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Contact: Kim YS
Plate: 23 row: L
Seq primer: SP6
Class: BAC ends.
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Best Local (
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JOURNAL
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BM773356
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                                                         FEATURES
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/note="Organ: Stometh; Vector: pTz18RP1; Site_1: ECORI; Site_2: Not1; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of 4 RNA higase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was circularized with E. coli DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The cDNA betained cDNA vectors were used for transformation of competent cells E. coli TOPIOF, by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonias in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded cDNAs prepared from original liberary and incubated with approach entity of the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli TopIOF' with electroporation method."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 IGCGTTCATCCCCGCATCCATGCACAACGCTCTAGCGCCCCATCTTCAGGATCAGCCTCCC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 CGCCCAGGTTCCTTTCTCCTCTGGCCCACTTCCTCATCTTTGTCTTCGTGACTTC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 CGAGCAGCATGGGAATGGAGGTGCGGGGCATGTTCACGATCAATTCCATTGGCCGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 522;
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                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="Lymphoblast-like"
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
mail: yongsung@mail.kribb.re.kr
Plate: 17 row: H column: 05
High quality sequence stop: 522.
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| QY 331 CACAACGCTCTAGCGCCCATCT | 462<br>391  | 542<br>451  | Db   602 ATCCCGGGGCGCTGATGTCCGC    Qy   506 ACCACCTGCGCCCAGAGATCC   Db   662 CCAACCTCGCCAGAAATCTT | 564<br>722<br>624<br>782                                       | RESULT 15 BB848859 LOCUS DEFINITION BB848859 RIKEN full-leng- ACCESSION BB848859 VERSION BB848859 VERSION BB848859 KEYWORDS SOURCE DOESNIEW Muse mouse. |   | Sciences Center(GSC), Yol<br>Sciences Center(GSC), Yol<br>The Institute of Physical<br>1-7-22 Suehiro-cho, Tsuri<br>Tel: 81-45-503-922<br>Fax: 81-45-503-922<br>Email: genome-res@gsc.ri)<br>URL:http://genome.gsc.ri)<br>Carninci,P., Shibata,Y.,<br>M., Konno,H., Okazaki,Y.,   | Normalization and subtraprepare full-length cDNA genes. Genome Res. 10 wagi, K., Fujiwake, S., II Watahiki, M., Yoneda, Y., S., Kawai, J., Okazaki, Y. Hayashizaki, Y.  | KIKKN Integrated sequences sequencing pipeline with 10 (11), 1757-1771 (2000). Konno, H., Fukunishi,Y., Y. and Hayashizaki,Y. Computer-based methods |
|-------------------------------|---|---|---|--|---|---|---|---|--|
|                               | 369 GGTGTTACACAGCGACACAGGCCAAAAACATCCCATGGCAGAATTACCATCTCAACGACTG 428<br> | 429 GAIGGAGGGITACCGCCACAITCCGGGACACITIGIGGCGTTCACGGGAIACCCGIG 488 | 489 CICCT 493<br>[    <br>518 CICCT 522   | 14 9   |   | cDNA<br>CDNA<br>DNA<br>Clon<br>found<br>Flate<br>High | Site_2: XhoI: cDNA made by oligo-dry priming.  Directionally cloned into Ecoli/XhoI sites using the following 5' adaptor: GGCACGAGGG. Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  143 a 325 c 262 g 165 t | Query Match  18.5%; Score 212.2; DB 10; Length 895;  Best Local Similarity 75.5%; Pred. No. 1.38-47;  Matches 342; Conservative 0; Mismatches 103; Indels 8; Gaps 6;  211 CTGCGGGCCATCACGATCCATTGGCCGGCTGGGGAACCAGATGGCCGAATAC 270  1 | GCCACACICTTIGCACTGGCCAGGATGAACGGACGCCCCCCCTGCGTTCATCCCCGCATCCATG   |
| qa                            | Qy<br>Db  | Qy<br>Db  | QY<br>Db  | RESULT 14 BE299719 LOCUS DEFINITION ACCESSION VERSION KEYWORDS | SOURCE<br>ORGANISM<br>REFERENCE<br>AUTHORS<br>TITLE<br>JOURNAL<br>COMMENT   | FEATURES  | BASE COUNT  | Query Masst Lo<br>Matches<br>Qy   | QY   |

T., Carninci, P., Furuno, M., Hanagaki, T., K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, K., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nowira, K., Numasaki, R., Okazaki, Y., Okidc, T., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa akaku-akahira, S., Tanaka, T., Tomaru, A., Toya, T. ishi, A., Muramatsu, M. and Hayashizaki, Y. f. Muramatsu, M. and Hayashizaki, Y. f. Muse, Full-length cDNAs (Akimura, T., et al. c.riken.go.jp,
c.riken.go.jp,
v. Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
ki,Y., Muramatsu,M. and Hayashizaki,Y.
ubtraction of cap-trapper-selected cDNas to
cDNA libraries for rapid discovery of new
10 (10), 1617-1630 (2000)
v. Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
ki,Y., Muramatsu,M., Inoue,Y., Kira,A. and 436 bp mRNA linear EST 26-NOV-2001 agth enriched, adult inner ear Mus musculus 5', mRNA sequence. Shibata, K., Itoh, M., Carninci, P., Sugahara 505 nce analysis (RISA) system--384-format h 384 multicapillary sequencer. Genome Res. ITCAGGATCAGCCTCCCGGTGTTACACAGGGGCC 390 541 TACCATCTCAACGACTGGATGGAGGAGGGTTACCGCCAC 450 601 -TGAAGGAGTTCACCCTGC-ATCACCACGTGCGGGAGGA 563 Exploration Research Group, RIKEN Genomic Tokohama Institute and Chemical Research (RIKEN) Irumi-ku, Yokohama, Kanagawa 230-0045, Japan TCTGCGGGTGAATGGGAGCCAGCCGAGTACTTTGTGGG 623 CTECAGGCCAAGTGGGCAGGCGACTTTCGTGG 781 ordata; Craniata; Vertebrata; Euteleostomi; lentia; Sciurognathi; Muridae; Murinae; Mus. CTTCACGGGAT-ACCCGTGCTCCTGGACCT---TCTACC CTATGTGCATGT 656 

for the mouse full-length cDNA

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Location/Qualifiers

1. 436
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/clone="1593004014"
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/clone="1593004014"
/clone="15930040101"
/clone="159004014"
/clone="15
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encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGGCCAGCGCCCAGGITCCTTTCTCTCTCTCTGGCCCACTTCCTCATCTTTGTCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.1%; Score 208.4; DB 10; Length 436; 81.9%; Pred. No. 9.7e-47; ive 0; Mismatches 41; Indels 22;
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                                                                                                                                                                        e mouse tissues
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Best Local Similarity
Matches 285; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107
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ORIGIN
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(without alignments)
1050.630 Million cell updates/sec
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
| SIDS2/gcgdata/geneseqgeneseqp-embl/AA1995.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
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                                                                                                                                                                                                                                                                                    US-10-040-863-8
2032
1 MASAQVPFSFPLAHFLIFVF......RSHFHLKAKGVTCYVAGRAF
                                                                                                                                                                     May 27, 2003, 14:52:27; Search time 48.1951 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS2/gcgdata/geneseg/genesegp-embl/AA1991.
/SIDS2/gcgdata/geneseg/genesegp-embl/AA1992.
/SIDS2/gcgdata/geneseg/genesegp-embl/AA1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDS2/gcgdata/geneseq/genesegp-embl/AA1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     908470
version 5.1.4_p5_4578 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
   GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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Searched:

Sequence:

Run on:

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997\_DAT:\*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998\_DAT:\*
/SIDS2/gcgdata/geneseqp-embl/AA1999\_DAT:\*
/SIDS2/gcgdata/geneseqy-eneseqp-embl/AA2000\_DAT:\*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001\_DAT:\*

/SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT:\* /SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT:\*

|           | Description              | Rat hobatoma H35 | Rat hepatoma #35 c | Rat hebatoma H35 c | Rat hebatoma H35 C | Porcine secretor t | Pig Secretor Sus | Human Secondaria | Human Seco catalot | GDP-Fuc:beta-D-dal | GDP-L-fucose-beta- |
|-----------|--------------------------|------------------|--------------------|--------------------|--------------------|--------------------|------------------|------------------|--------------------|--------------------|--------------------|
| SUMMARIES | ID                       | AAB36104         | AAE16622           | AAB36105           | AAE16623           | AAW37855           | AAW53101         | AAW69332         | AAB36106           | AAR13751           | AAR80154           |
|           | OB                       | 21               | 23                 | 21                 | 23                 | 19                 | 19               | 13               | 21                 | 12                 | 16                 |
|           | Duery<br>Match Length DB | 380              | 380                | 353                | 353                | 340                | 340              | 343              | 344                | 365                | 365                |
| œ         | Query                    | 100.0            | 100.0              | 93.3               | 93.3               | 73.9               | 73.9             | 73.1             | 72.6               | 52.0               | 52.0               |
|           | Score                    | 2032             | 2032               | 1896               | 1896               | 1502               | 1502             | 1485.5           | 1475               | 1057.5             | 1057.5             |
|           | Result<br>No.            | ٦                | 7                  | m                  | 4                  | ហ                  | Ø                | 7                | ထ                  | 6                  | 10                 |

|  | cosyltransfer<br>transferase<br>lpha-1-2 fuc<br>alpha (1,2) | alpha-<br>vis al<br>secret<br>ori UA                     | eroides in<br>conibacter<br>protein<br>h Factor<br>legans alp<br>l'human di | uman dia<br>olypepti<br>inding-p<br>and neur<br>and neur<br>and neur | acta sequen<br>onibacterium<br>yromonas gen<br>protein seg<br>signal tran<br>genesis asso |
|--|---|--|---|--|---|
| AAR70422<br>AAR70421<br>AAR90572<br>AAW23805<br>AAW13640<br>AAY97279 | AAR45936<br>AAW53102<br>AAY79302<br>AAB47995<br>AAW97356    | AAW30630<br>AAY17969<br>AAG03530<br>AAY92713<br>AAG64071 | AAAN31592<br>AAR39722<br>AAR26061<br>AAY70408<br>ABG10624<br>ABG10624       | ABG28599<br>AAM93762<br>AAB16426<br>AAU11814<br>AAU11817<br>AAU11816 | AAU461993<br>AAB61993<br>AAB93020<br>AAU17082<br>AAE11890                                 |
| 16<br>17<br>17<br>18<br>18   | 15<br>19<br>23<br>20<br>20                                  | 221120   | 2221322   | 7333555  | 755<br>755<br>755<br>755<br>755<br>755<br>755<br>755<br>755<br>755                        |
| 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3                                | 365<br>365<br>365<br>365                                    | 365<br>357<br>110<br>300<br>300                          | 661<br>690<br>317<br>355<br>1515<br>402                                     | 1073<br>984<br>2008<br>2306<br>2352<br>586                           | 604<br>353<br>394<br>1031<br>2057   |
|  |   | 100000   | 0   |  |   |
| 1057.5<br>1057.5<br>1057.5<br>1057.5<br>1057.5                       | 049.<br>046.<br>046.<br>046.                                | 044.<br>99.<br>328.<br>14.<br>14                         | , ,   | 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                | · · ထ ထ ထ ထ ထ   |
| 11<br>12<br>13<br>14<br>15   | 17<br>18<br>20<br>21<br>21                                  | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                    | 335<br>335<br>335<br>335<br>335<br>335<br>335<br>335<br>335<br>335          | 1 8 8 8 8 8 4<br>4 13 9 7 8 9 9                                      | 4444  |

## ALIGNMENTS

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Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease; small cell lung carcinoma.
                                                                            Rat hepatoma H35 cell alphal-2fucosyltransferase.
                                                                                                                                                                                                                                                  (PACI-) PACIFIC NORTHWEST CANCER FOUND.
               AAB36104 standard; Protein; 380 AA.
                                                                                                                                                                                                             99WO-US07384.
                                                                                                                                                                                                                              99WO-US07384
                                                        (first entry)
                                                                                                                                                                                                                                                                      Holmes EH, Sherwood AL;
                                                                                                                                                                                                                                                                                         WPI; 2000-687262/67.
N-PSDB; AAC67965.
                                                                                                                                                Rattus norvegicus.
                                                                                                                                                                  WO200064464-A1.
                                                                                                                                                                                                           23-APR-1999;
                                                                                                                                                                                                                              23-APR-1999;
                                                         19-FEB-2001
                                                                                                                                                                                        02-NOV-2000.
                                     AAB36104;
RESULT 1
        AAB36104
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New rat ganglioside GM1-specific alphal-2Fucosyltransferase, useful for

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                                                       The present sequence was given in a specification relating to an isolated trat gangloside GM_1:specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-2calbetal-3GalNAc, a glycolippid, glycoprotein, glycolipportein or a free oligosaccharide comprising fucalphal-2dalbetal-3GalNAc. The method involves contacting alphal-2dalbetal-3GalNAc. The method involves contacting alphal-2dalbetal-3GalNAc. The which GDP fucose and a molecule or glycolippid, glycolipportein or oligosaccharide having a terminal by contacting the protein with GDP-fucose and ganglioside GM_1. The by contacting the protein with GDP-fucose and ganglioside GM_1. The bottal-3GalNAc glycolipporteins, glycolipporteins, glycolippids and ganglioside and fucosyl-GM_1 is useful for inducing an immunocherapeut. Or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
useful as a nutritional composition
neurological diseases -
                                                                                                                                                                                                                                                                                                                                                           RDSEQHGNGELRGMFTINSIGRLGNOMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFGIWAAXLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLKALTPACP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat; alphal-2fucosyltransferase; alphal-2FucT; antisense therapy; galactose betal-3N-acetylgalactosamine; Galbetal-3GalNAc; glycolipid; glycoprotein; glycolipoprotein; oligosaccharide; fucosyl-GM1; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GM1; cell transformation
                                                                                                                                                                                                                                                                                                            1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMITQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                                                                 1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LHDHVREBAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                                                                                                                                                                           SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT
                                                                                                                                                                                                                                                              Score 2032; DB 21; Length 380;
Pred. No. 1.7e-212;
Mismatches 0; Indels 0:
preparation of fucosyl GM1 which is or immunotherapeutic for cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H35 cell alphal-2FucT.
                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE16622 standard; Protein; 380
                                                                                                                                                                                                                                                               100.0%;
                                Claim 1; Fig 5; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSHFHLKAKGVICYVAGRAF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                        380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat hepatoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-APR-2002
                                                                                                                                                                                                                                                                           Best Local Sim
Matches 380;
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE16622;
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AAE16622
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The invention relates to rat GMI-specific alphal-2fucosyltransferase
(alphal-2FucT) enzyme and its corresponding nucleic acid. This nucleic
acid is specific for a carbohydrate moiety found in ganglioside GMI,
acid is specific for a carbohydrate moiety found in ganglioside GMI,
acid is specific for a carbohydrate moiety found in ganglioside GMI,
acteminal galactose betal-3N-acetylgalactosamine (Galbetal-3GalNAC)
saccharide. Alphal-2FucT DNA is useful for producing rat alphal-2FucT
protein by recombinant techniques. Alphal-2FucT DNA is useful for the
protein by recombinant techniques. Alphal-2FucT DNA is useful for detecting oncogenic transformation which
alphal-2FucT DNA is useful for detecting oncogenic transformation which
involves assaying for changes in expression of alphal-2 FucT. Since
alphal-2FucT is activated in cell transformation, antisense sequences
derived from alphal-2FucT DNA is useful in gene therapy and
cor treating cancer. Alphal-2FucT DNA is useful in gene therapy and
characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for producing GMI-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
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                            /note= "Intracellular/Transmembrane domain"
199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                   Mismatches
                                                                                           /note= "N-glycosylated"
                                                                                                                                                                                                                                              /note= "N-glycosylated"
                                                                                                                                                                                                  /note= "N-glycosylated"
location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0298886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NWHO-) NORTHWEST HOSPITAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sherwood AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-121132/16.
N-PSDB; AAD27207.
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                                                                    Modified-site
                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Simmatches 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holmes EH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
Key
Domain
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241 FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300

301 301 361 361

g Óγ g ŏ Db RESULT 3

207 180 267 327

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Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for producing GM1-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues
                                                                                                                                                                                                                                            241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTYLANYTLFDSPF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat; alphal-2fucosyltransferase; alphal-2fucT; antisense therapy; galactose betal-3N-acetylgalactosamine; Galbetal-3SalNac; glycolipid; glycoprotein; glycolipoprotein; oligosaccharide; fucosyl-GMI; cancer; gene therapy; oncogenic transformation; cytostatic; ganglicside; GMI; cell transformation; catalytic domain.
GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER
                     GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER
                                                                                           GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                        YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
                                                                                                                                                                RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                                                                                                                                                                               LKVFKPEAAFLPEWVGIPADLSPLLKALIPACPRSHFHLKAKGVTCYVAGRAF 380
                                                                                                                                                                                                                                                                                                                  /note= "Region which overlaps rat FTB"
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H35 cell alphal-2FucT catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172
/note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-glycosylated"
266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAE16623 standard; Protein; 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Fig 3; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0298886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NWHO-) NORTHWEST HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holmes EH, Sherwood AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-121132/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD27208
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat hepatoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE16623;
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88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is given in a specification relating to a rat ganglioside GM_1-specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-2galbetal-3galNac, a glycolipid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising Fucalphal-2galbetal-3galNac. The method involves contacting alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoprotein, glycolipoprotein or oligosaccharide having a terminal Galbetal-3galNac group. It is also useful for synthesis of fucosyl-GM_1 by contacting the protein with GDP-fucose and ganglioside GM_1 The obtained glycoproteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
       TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACP 360
                         Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycolipoproteins, glycolipids and oligosaccharides are useful as nutritional compositions and fucosyl-GM_1 is useful for inducing an immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carchnoma.
                                                                                                                                                                                                                                                                                                                          Rat hepatoma H35 cell alphal-2fucosyltransferase catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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100.0%; Pred. No. 1e-197;
ive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PACI-) PACIFIC NORTHWEST CANCER FOUND.
                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                  AAB36105 standard; Protein; 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 3A; 91pp; English.
                                                                                                       RSHFHLKAKGVTCYVAGRAF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US07384
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                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            small cell lung carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 353; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sherwood AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-687262/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200064464-A1.
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                                                                                                                                                                                                                                                      AAB36105;
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The invention relates to rat GMI-specific alphal-2fucosyltransferase (alphal-2rur) enzyme and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate moiety found in ganglioside GMI, a terminal galactose betal-3M-acetylgalactosamine (Galbetal-3GalNAc) saccharide. Alphal-2rur DNA is useful for producing rat alphal-2rur protein by recombinant techniques. Alphal-2rur DNA is useful for the preparative synthesis of fucosyl containing glycolipids, glycoproteins, glycollipoproteins and oligosaccharide, and for preparing fucosyl-GMI. Alphal-2rur DNA is useful for detecting oncogenic transformation which involves assaying for changes in expression of alphal-2rur. Since alphal-2rur DNA is useful for inhibiting, suppressing curvated from alphal-2rur DNA are useful for inhibiting, suppressing antisense therapy. The present sequence is rat hepatoma H35 cell
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                                                                                                                                                                                                                                                                                                                                                                                                                   207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 327
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                            87
                                                                                                                                                                                                                                                                                                                                       LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secretor; glycosyltransferase; FUT2; pig; epitope; antigen; transgenic animal; xenotransplantation; organ transplant.
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-terminal cytoplasmic tail"
                                                                                                                                                                                                                                                                         93.3%; Score 1896; DB 23;
100.0%; Pred. No. 1e-197;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Asn is N-qlycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "C-terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porcine secretor transferase (FUT2).
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/note= "C
185..187
/note= "As
                                                                                                                                                                                                                                                                                                         Matches 353; Conservative
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                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                353 AA;
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                                                                                                                                                                                                                                                Sequence
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This polypeptide comprises porcine secretor glycosyltransferase

(SE or FUI2), a type II integral membrane protein has high affinity

(SE or FUI2), a type II integral membrane protein has high affinity

(Cor type I and type III substrates. Its amino acid sequence was

deduced from the nucleotide sequence of a genomic DNA clone (see

AAV29003) isolated from a pig Ilver library on the basis of homology

(Cor thuman FUI2 cDNA. Pig FUI2 shows 83.2% identity with human FUI2.

Expression of a glycosyltransferase, such as porcine Se, in a

tissue results in reduced expression of unwanted carbohydrate

c pitopes on the tissue, especially porcine heart, liver, kidney or

pancreas, rendering if more suitable for transplantation, i.e. less

immunogenic and of increased immunological acceptability. A

claimed method of producing a cell from a donor species that is

immunologically acceptable to a recipient species sinvolves reducing

levels of carbohydrate on the donor cell that causes it to be

recognised as non-self by the recipient by expressing a nucleic

acid for a glycosyltransferase such as porcine Se in the cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RDSEQHGNGELRGMFTINSIGRLGNQMGEXATLFALARMNGRLAFIPASMHNALAPIFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 -----SSPQLKGMWTINAIGRLGNQMGEYATLYALARMNGRPAFIPPEMHSTLAPIFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG
                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding glycosyltransferase able to compete with second such enzyme - particularly used to reduce expression of unwanted carbohydrate epitope(s) on tissues intended for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGÌPADLSPLLK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.9%; Score 1502; DB 19; Best Local Similarity 79.6%; Pred. No. 9.1e-155; Matches 281; Conservative 28; Mismatches 30;
                    /note= "Asn is N-glycosylated" 305..307
                                                         /note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Fig 1A-B; 40pp; English.
                                                                                                                                                                              97WO-AU00540.
                                                                                                                                                                                                                     96AU-0001823,
                                                                                                                                                                                                                                                                                                Sandrin MS;
279..281
                                                                                                                                                                                                                                                         (AUST-) AUSTIN RES INST.
                                                                                                                                                                                                                                                                                                                                     WPI; 1998-169148/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 AA;
                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV29003
                                                                                                                                                                                                                                                                                            McKenzie IFC,
  Modified-site
                                    Modified-site
                                                                                                                                                                                                                  23-AUG-1996;
                                                                                                WO9807837-A1
                                                                                                                                     26-FEB-1998
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PRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                        LOWE
                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              28-FEB-1995;
                                                                                                                                                                                                                                                                                                                                        28-FEB-1995;
                                                                                                                                                                       20-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                    (GIOR/) (KELL/) F (LENN/) I
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                                                                                                     RESULT 7
AAW69332
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                                                                                                                                                              XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents pig secretor used in an example of the present invention. The present invention describes nucleic acids (NA) encoding a chimeric glycosyltransferase. The NAs comprises a catalytic domain of a first glycosyltransferase (GT) and a localisation signal of a second GT, whereby when the NA is expressed in a cell and where the cohimeric enzyme is located in an area of the cell where it is able to compete for substrate with a second GT, resulting in reduced levels of a product from the second GT. The NAs can be used to produce cells and organs with desired glycosylation patterns. Products and methods of the present invention can be used to reduce the levels of undesirable epitopes in cells, tissues or organs which may be used in transplantation or gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLSMQASFFFPTGPFILFVFTASTIFHLQQRMVKIQP--TWELQMVTQVT---TESP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding chimeric glycosyltransferases - used for altering carbohydrate levels on the surface of cells, useful in therapy and transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 340;
                                                                                                                          secretor; chimeric; glycosyltransferase; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.9%; Score 1502; DB 19;
79.6%; Pred. No. 9.1e-155;
iive 28; Mismatches 30;
                                AAW53101 standard; Protein; 340 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 6; 51pp; English.
                                                                                                                                                                                                                                                     96US-0024279.
                                                                                                                                                                                                                               97WO-AU00492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 73.9%
Best Local Similarity 79.6%
Matches 281; Conservative
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                 Sandrin MS;
                                                                                                                                                                                                                                                                                         (AUST-) AUSTIN RES INST.
                                                                                                                                                                                                                                                                                                                                      WPI; 1998-159170/14.
N-PSDB; AAV21639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 AA;
                                                                                                                                       transplantation.
                                                                                                                                                                                                                                                                                                                McKenzie IFC,
                                                                                                                                                                                  WO9805768-A1
                                                                                                                                                                                                                               01-AUG-1997;
                                                                                                                                                                                                                                                       21-AUG-1996;
                                                                                                                                                                                                                                                                 02-AUG-1996;
                                                                            08-JUL-1998
                                                                                                                                                                                                          12-FEB-1998
                                                                                                                                                            Sus scrofa.
                                                       AAW53101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
          RESULT 6
                     AAW53101
                                                                                                               Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sec2; alpha(1,2) fucosyltransferase; H blood group; secretor genotyping; GDP-L-fucose;beta-D-galactoside 2-alpha-L-fucosyltransferase; human;
STSKALGPSQLRGMWIINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAM--WELPV------QIPVLA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPENR 6C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or nonsecretor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19, Length 343;
                                                                                                                producing
                                                                                  TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secretor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rouguier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.1%; Score 1485.5; DB 1
77.9%; Pred. No. 5.8e-153;
ive 30; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant enzyme and genotyping person as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lowe JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Column 45-50; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding fucosyltransferase enzyme
                                                                                                                                                                                                                                                                                     AAW69332 standard; Protein; 343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lennon G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUT2; nonsecretor genotyping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0395800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Sec2 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0395800
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 73.1
Best Local Similarity 77.9
Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Giorgi D, Kelly RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-520127/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIORGI D.
KELLY R J.
LENNON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROUQUIER S
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Query Match

344 AA;

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230 WFRARXSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTI 289
                                                                                                                                                        RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                 50 STSKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI 109
                                                                                                                                                                                                                                        SLPVLHSDTAKKIPWQNYHLNDWMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEF 179
                                                                                                     Gaps
                                                                            MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The amino acid sequence codes for a protein capable of functioning as a GPP- Fuc:[beta-D-Gal alpha(1,2)- fucosyltransferase. The functional protein is represented by amino acids 33 to 365. The enzyme produced by the DNA sequence can be used in enzymatic fucosylation of chain-terminating galactose residues on lactosemine or neolacto type beta-D-galactoside to alpha-2-L-fucose residues. See also AAR13749-R13752.
                                                                                                                                                                                                                                                           TLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALD
                                                                                                                                                                                                                                                                                                                                                                                                    240 MFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343
                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characteristic
oligo or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIFGIWAAYLAGGDIIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase
              Pred. No. 8.1e-152;
); Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolation of gene conveying post-translational e.g. the presence of soluble or membrane bound polysaccharide or glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
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AAR23751 standard; Protein; 365
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90US-0479858.
90US-0480133.
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                Best Local Similarity 77.7
Matches 275; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycosyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAR13751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-1991;
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14-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9112340-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR13751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lowe JB;
                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is given in a specification relating to a rat ganglioside GM_1-specific alphal-2fucosyltransferase protein. The protein of its useful for synthesis of a molecule comprising Fucalphal-2dalbetal-3dalNac. a glycolipid, glycoprotein, glycolipoprotein, glycolipoprotein, glycolipoprotein, glycolipoprotein, glycolipoprotein or a free oligosaccharide comprising Fucalphal-2dalbetal-3dalNac.

The method involves contacting alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoprotein, glycolipoprotein or oligosaccharide protein or coligosaccharide glober fucosyl-GM_1 by contacting the protein with claps and ganglioside GM_1. The obtained glycoproteins, glycolipoproteins, glycolipoproteins, glycolipoproteins, glycolipoproteins, glycolipids and glocosyl-GM_1 is useful for inducing an immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rat ganglioside GML-specific alphal-2Fucosyltransferase, useful for sparation of fucosyl GML which is useful as a nutritional composition immunotherapeutic for cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Sec2; alphal-2fucosyltransferase; cytostatic;
neuroprotective; nootropic; gene therapy; Fucalphal-2calbetal-3GalNAc;
immunotherapy; immunosuppression; cancer; neurological disease;
small cell lung carcinoma.
                                                    240
                                                                                                                                                                                                            FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
                             SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
                                                                                                                                LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                                            353
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                                                                                                                                                                                                                                                                                             TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
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(PACI-) PACIFIC NORTHWEST CANCER FOUND.

23-APR-1999; 33-APR-1999;

Holmes EH, Sherwood AL; WPI; 2000-687262/67

99WO-DS07384 99WO-US07384

WO200064464-A1.

02-NOV-2000

Homo sapiens

Example; Fig 3B; 91pp; English.

New rat gang preparation

AAB36106 standard; Protein; 344 AA

RESULT 8

230

Db δÿ g

301

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290

Human Sec2 catalytic domain

(first entry)

19-FEB-2001

AAB36106;

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GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase (Fuc-T) is encoded by cDNA (AAO98461) isolated from a human epidermal carcinome cell line. The enzyme is responsible for the synthesis of 2'-fucosyllactose, one of the oligosaccharides in human milk. Other products of Fuc-T include glycoprofisms contg. beta-linked terminal galactose residues which can be fucosylated by Fuc-T. This DNA can be used to produce non-human transgenic mammals able to produce secondary gene products, e.g. oligosaccharides, in their milk. The transgenic mammals milk biochemically resembles human milk. This humanised milk can be used in the prepn. of an enteral nutritional product useful in the nutritive maintenance of an animal.
                                                                                                                                                                                                                                                                                                                                                                                                               57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                          71 P-----QH-PASLSGIWTVYPNGRFGNQNGQYATLLALAQLNGRRAFILDAMHAALAP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|||:|||| : :||:||| : 183 VFRITLPVLAPEVDSRIPWRELQLHDWMSEEYADLRDPFLKLSGFPCSWTFFHHLR3GIR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWYGIPADLSPLLXA 354
                                                                                                                                                                                                                                                                                                                                                                            11 LAFLLVCVLSVIFFLHIHODSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC
                                                                                                                                                                                                                                                                                                                                                 --RIVKLQPLSEKELPMTTQMSSGNTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycosyltransferase; glycosylation; oligosaccharide; glycoprotein; glycolipid; transgenic animal; cattle; milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase;
                                                                                                                                                                                                                                                                                                              87; Indels
                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                           ; Score 1057.5; DB 1; Pred. No. 3.1e-106; 46; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR70422 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                        52.0%;
                                                                                                                                                                                                                                                                                                                                             12 LAHFLIFVFVTSTIIHLQQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0208889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2-Alpha-fucosyltransferase.
                                                                                                                                                                                                                                                                                          Best Local Similarity 56.5
Matches 205; Conservative
                                                                                                                                                                                                                                         365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 AKP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 LTP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                          Query Match
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            δ
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                                                                                                                                                                                             117 IFRISLPVLHSDTAKKIPWQNYHLNDWMEBRYRHIPGHFVRFTGYPCSWTFYHHRRPEIL 176
                                                                                                                                                                                                                                                                :|||:|||| : :||:||| : 133 VFRITLEVLAPENDSRIPWRELQLHDWMSEEYADLRDFIKLSGFPGSWTFFHHLREQIR 182
                                                                                                                                                                                                                                                                                                              177 KEFTLADHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL 234
                                                                                                                                                                                                                                                                                                                                                                                   235 EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH 294
                                                                                                                                                                                                                                                                                                                                                                                                      295 TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWGIPADLSPLLKA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                   11 LAFLLVCVLSVIFFLHIHODSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase; Fuc-T; synthesis; 2'-fucosyllactose; oligosaccharide; human milk; non-human transgenic mammal; secondary gene product.
                                                                                                       ---RIVKLQPLSEKELPMTTQMSSGNTES
                                                                                                                                                                       PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARNNGRLAFIPASMHNALAP
                                                                                                                                                                                                                                                                                                                                    Prodn. of human:ised milk by non-human transgenic mammal - by inserting heterologous gene encoding human catalytic entity which produces oligo:saccharide(s) and glyco:conjugate(s) into mammal's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDP-L-fucose-beta-D-galactosidase alpha-1,2-fucosyltransferase.
                                         Length 365;
                                                                       87; Indels
                                    DB 12;
                                    ; Score 1057.5; DB 12; Pred. No. 3.1e-106; 46; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mukerji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Moreman KW,
Smith DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 62-54; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; Protein; 365 AA.
                                    52.0%;
56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95WO-US00926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                 Local Similarity 56.5
nes 205; Conservative
                                                                                                      LAHFLIFVFVTSTIHLQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kopchik JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cummings RD, Kopc.....TM, Prieto PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-336739/43.
 365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ABBO ) ABBOTT LAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JAN-1995;
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Sequence
                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR80154;
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                                                                                                                                                                       57
                                                                 Matches
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AAR80154

7.0

Length 365;

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4
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                                                                                                                                                                                                                                                                                                                                                                                                                      IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
                                                                                                                                                                                                                                                                                                                                                                                                                                                    182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New transgenic non-human mammal milk prods - contg. heterologous components produced as secondary gene prods. of an heterologous gene
                                                                                                                                                                                                                                                                                           25; Gaps
                                                                                                                                                      2-Alpha-fucosyltransferase (AAR70422) is encoded by a cDNA clone (AAR01083) isolated from a human epidermal carcinoma A431 library. The enzyme can be expressed in the milk of a transgenic mammal, esp. cow. This allows large-scale prodn. of oligosaccharides and glycosylated proteins and lipids in the milk.
                                                                                                                                                                                                                                                                                                                                                                                   KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA
                                                                                                                                                                                                                                                                                                                12 LAHFLIFVFVTSTIIHLQQ------RIVKLQPLSEKELPMTTQMSSGNTES
                                                                                                                                                                                                                                                                                                                                          11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase;
glycosyltransferase; oligosaccharide; glycoprotein; glycolipid;
transgenic animal; cattle; glycosylation; milk.
                                                                                                                                                                                                                                                                 16; Length 365
                                                                                                                                                                                                                                                                                           87; Indels
                                                                                                                                                                                                                                                              52.0%; Score 1057.5; DB 16 56.5%; Pred. No. 3.1e-106; iive 46; Mismatches 87;
               Mukerji
                                                                                         mammal milk prods
             f, Moremen KW,
Smith DF;
                                                                                                                             Example 1; Page 62-64; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR70421 standard; Protein; 365 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
            Kopchik JJ,
                                                                                                                                                                                                                                                                           Best Local Similarity 56.5
Matches 205; Conservative
                                                                                          New transgenic non-human
                          Pierce JM, Prieto PA,
                                                  WPI; 1995-328284/42.
                                                                                                                                                                                                                                     365 AA;
                                                                  N-PSDB; AAT01083
               Cummings RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                     Seguence
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                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                      117
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117 IFRISLPVLASDTAKKIPWQNYHLNDWMEBRYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 1,76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               ---RIVKLOPLSEKELPMTTQMSSGNTES 56
                                                                                                                                                                                                                                                         Alpha-1,2-fucosyltransferase (AAR70421) is encoded by a cDNA clone (AAT01082) isolated from a human epidermal carcinoma cell line A431 cDNA library. The enzyme can be expressed in the milk of a transgenic mammal, esp. cow. This allows large-scale prodn. of oligosaccharides or glycosylated proteins and lipids in the milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 RQAMDWFRARHEAPVFVVTSNGMEWCKENIDISQGDVTFAGDGQEATPWKDFALLTQCNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA
                                                                                                                                                                                             i.i
                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H-transferase; xenograft hyperacute rejection; transplantation; glycosyltransferase; galactose alpha(1,3) galactose.
                                                                                                                                                           Transgenic animal expressing heterologous catalyst - used in metabolite prodn esp. glycosyltransferase for prodn. of oligosaccharide(s) and glyco-conjugate(s) in the milk, useful foods, pharmaceuticals, etc.
                                                                                                                                                                                                                                                                                                                                                                       52.0%; Score 1057.5; DB 16; Length 56.5%; Pred. No. 3.1e-106; Live 46; Mismatches 87; Indels
                                                                              J, Moremen KW, Mukerji
Smith DF;
                                                                                                                                                                                                                                  Example 1; Page 62-64; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 365 AA.
95WO-US01147
                        94US-0209132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 56.5
Matches 205; Conservative
                                                                               Kopchik JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                              LAHFLIFVFVTSTIIHLOO-
                                                                                              Prieto PA,
                                                                                                                      WPI; 1995-328279/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human H-transferase.
                                                    (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR90572 standard;
                                                                                                                                                                                                                                                                                                                                           365 AA;
                                                                                                                                     N-PSDB; AAT01082
24-JAN-1995;
                        09-MAR-1994;
                                                                               Cummings RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357
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                                                                                              Pierce JM,
                                                                                                                                                                                                                                                                                                                                              Seguence
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Best Local Similarity Matches 205; Conserv
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                                                                                                                                                                               11-JUL-1994;
                                                                                                                       Homo sapiens
                                                                                                                                                                                                  11-JUL-1994;
                15-SEP-1997
                                                                                                                                        US5625124-A.
                                                                                                                                                           29-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                        Falk P,
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                                                                                                                                                                                                                                         The human H-transferase (AAR90572) product of a cDNA clone (AAT12238) prepd. from human epidermoid carcinoma cells (ATCC CRL 155 A-431) can be expressed in xenogeneic organs, tissues and cells using a vector such as pAPEx-1 (AAT1239). This results in decreased expression of the non-human antigen galactose alpha(1.3) galactose on the surface of the organs etc. so that hyperacute rejection is reduced upon transplantation to humans.
                                                                                                                                                                                                                                                                                                                                                                                                                    57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEXATLFALARMNGRLAFIPASMHNALAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                117 IFRISLPVLHSDTAKKIPWQNYHLNDWMERRYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKALDMFRARYSSPVFVVISNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 LAFLLVCVLSVIFFLHIHODSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
                                                                                                                                                                                                                                                                                                                                                                                  -----RIVKLQPLSEKELPMTTQMSSGNTES 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL
                                                                                                                                                                            Redn. of rejection of xenogeneic cells following transplantation by introducing a vector expressing fucosyl:transferase into the cells
                                                                                                                                                                                                                                                                                                                                            DB 17; Length 365;
                                                                                                                                        Squinto SP;
                                                                                                                                      Sandrin MS,
                                                                                                                                                                                                                                                                                                                                          52.0%; Score 1057.5; DB 1756.5%; Pred. No. 3.1e-106; Live 46; Mismatches 87;
                                                                                                                                      Rother RP,
                                                                                                                                                                                                                         Example 1; Page 45-47; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW23805 standard; Protein; 365 AA.
                                                                            94US-0278282
                                                         95WO-US07554
                                                                                     94US-0260201
                                                                                                      (ALEX+) ALEXION PHARM INC (AUST-) AUSTIN RES INST.
                                                                                                                                                                                                                                                                                                                                                                               12 LAHFLIFVFVTSTIIHLQQ-
                                                                                                                                     Mckenzie IFC,
                                                                                                                                                                                                                                                                                                                                                             205; Conservative
                                                                                                                                                       WPI; 1996-049326/05
                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                        365 AA;
                                                                                                                                                              N-PSDB; AAT12238
                                                                           21-JUL-1994;
                  WO9534202-A1
                                                        14-JUN-1995;
                                                                                    15-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 LTP 357
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                                     21-DEC-1995
                                                                                                                                   Fodor WL,
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A claimed transgenic mouse expresses, in its intestinal epithelial cells, the enzyme human GDP-L-fucose.beta-D-galactoside 2-alpha-L-fucosyltransferase (also called alpha 1.2 FT) or human GDP-L-fucose.beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase (also called alpha 1.3/4 FT). The enzyme is expressed under the control of a qut epithelial cell-specific promoter and Helicobacter pylori adheres to the transgenic cells. The transgenic mouse and intestinal epithelial cells from it are useful as models for screening compounds for the ability to inhibit adhesion of H. pylori to gut epithelial cells. The present sequence represents human alpha 1.2 FT and was published by Larsen et al., proc.Natl.Acad.Sci.USA, 87:
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                                                                                                                                                                                                                                                                                Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----RIVKLQPLSEKELPMTTQMSSGNTES
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transgenic mouse expressing human enzyme promoting intestinal
                                                                                                                                                                                                                                                                                                                                              alpha 1,2 FT; transgene; transgenic mouse; animal model; intestinal adhesion; Helicobacter pylori infection; stomach; small intestine; gut, epithelial cell; surface receptor; carbohydrate antigen; gastritis; peptic ulcer; neoplasia; gastric adenocarcinoma; Lewis antigen; fucosylation.
                                                                                                                                            Human alpha 1,2 fucosyltransferase (EC 2.4.1.69).
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(first entry)
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TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA 354
            PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 LAHFLIFVFVTSTIIHLQQ------RIVKLQPLSEKELPMTTQMSSGNTES 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human GDP-Puc:beta-D-galactoside alpha(1,2)-fucosyltransferase (AAW13640) is an enzyme involved in the expression of type I and II blood group H structures. Its amino acid sequence was deduced from an isolated DNA (AATG1677) derived from human A431 cells. Expression of the fucosyltransferase animal cell lines provides specific capabilities with respect to post-translational modification of the oligosaccharides of expressed proteins or lipids. Specific applns. of the enzyme include enzymatic fucosylation of chain-terminating galactose residues on lactoseamine or neolacto type beta-D-galactoside to alpha-2-fucose residues. The enzyme can also be used to raise antibodies as diagnostic reagents and to screen cpds. for fucosyltransferase inhibitor activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant fucosyltransferase proteins - useful for modifying cell surface oligosaccharide structures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.0%; Score 1057.5; DB 18; Length 365; 56.5%; Pred. No. 3.1e-106; ive 46; Mismatches 87; Indels 25;
                                                                                                                                                                                                                                                  Alpha(1,2)-fucosyltransferase; glycosylation; oligosaccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 280-281; 329pp; English.
                                                                                                                                                                                                                         Human alpha(1,2)-fucosyltransferase.
                                                                                                                                          AAW13640 standard; Protein; 365 AA.
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es 205; Conserv
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                                                  LTP 357
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(without alignments)
715.625 Million cell updates/sec
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US-09-254-077A-12

US-08-395-800A-10

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version :
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| 10 000 000 00 00 00 00 00 00 00 00 00 00 | 05-08-780-30 | US~09-390-131-5 | US-07-906-349A-6 | US-08-220-151-22 | US-08-413-118-22 | US-08-473-446-22 | 5470718-3 | US-08-167-035-6 | US-08-208-887A-6 | 08-08-539-005-6 | US-08-815-176-3 | US-08-815-176-4 | US-08-664-962B-6 | US-09-311-743-6 | US-09-280-598-6 | US-09-197-344-3 | US-09-197-344-4 |  |
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| 000                                      | 7            | 30              | 31               | 32               | 33               | 34               | 32        | 36              | 37               | 38              | 39              | 40              | 41               | 42              | 43              | 44              | 45              |  |

## ALIGNMENTS

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Query Match
Best Local Similarity 79.68
Matches 281; Conservative
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                                 Query Match
Best Local Sim:
Matches 281;
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US-09-254-077A-6
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                                                                             Sequence 10, Application US/09298886
Patent No. 632970
GENERAL INFORMATION:
TITLE OF INVENITON: GAL-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENITON: GAL-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENITON: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT APPLICATION NUMBER: US/09/298,886
NUMBER OF SEQ ID NOS: 29
SEQ TWARE: Patentin Ver. 2.0
SEQ ID NO 10
SEQ ID NO 10
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APPLICANT: SANDERIA, MAURO S.
TITLE OF INVENTION: UNCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562-505W0
CURRENT FILING DATE: 1999-06-11
PRIOR PILING DATE: 1999-06-12
PRIOR PLICATION NUMBER: POT/AU97/00540
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-23
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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100.0%;
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; ORGANISM: Rattus norvegicus
US-09-298-886-10
 361 RSHFHLKAKGVTCYVAGRAF
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TYPE: PRT
ORGANISM: Sus scrofa
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APPLICANT: MCKENZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.50300
CURRENT PALICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VOIS: 12
SOFTWARE: PATENTIN VOI: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                    181 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
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                                              14;
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                                              Indels
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73.9%; Score 1502; DB 4;
79.6%; Pred. No. 5.1e-165;
iive 28; Mismatches 30;
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79.6%; Pred. No. 5.1e-165;
Live 28; Mismatches 30;
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us-10-040-863-8.rai

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Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                      RESULT 6
US-09-254-077A-8
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                                                                                                                                                                                                                                    APPLICANT: ROUGOIER, SYLVIE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: GIORGI, DOMINIQUE
TITLE OF INVENTION: GDP-L-PUCOSE: BETA-D-CALACTOSIDE
TITLE OF INVENTION: 2-ALPHA-L-PUCOSYLITRANSFERASES, DNA SEQUENCES ENCODING THE
TITLE OF INVENTION: SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
TITLE OF INVENTION: GENOTYPING A PERSON
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                 TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 353
                                                                          DB 1; Length 343;
                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.1%; Score 1485.5; DB 1; 77.9%; Pred. No. 4.2e-163; tive 30; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US/08/395,800A
28-FEB-1995
                                                                                                                                                                Sequence 8, Application US/08395800A
Patent No. 5807732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELES: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         APPLICANT: LOWE, JOHN B
APPLICANT: LENNON, GREGORY
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Best Local Similarity 77.9%
Matches 275; Conservative
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FILING DATE: 28-FEB
CLASSIFICATION: 435
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                                                                                                                                                                                  Patent No.
                            227
241
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Sequence 11, Application US/0929886

GENERAL INFORMATION:

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAI GANGLICSIDE

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/298,886

CURRENT FILING DATE: 1999-04-26
                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: SANDERLY, MAURO S.
APPLICANT: MCKENELE, IAN C. F.
IITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT
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CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: PCT/AU97/00540
PRIOR PILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: PO 1823
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver: 2.1
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Query Match 53.5%
Best Local Similarity 57.6%
Matches 209; Conservative
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Patent No. 6399758
GENERAL INFORMATION:
APPLICANT: SANDRIN, MAURO S.
APPLICANT: MCKENZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRAIE EPITOPES
FILE REFERENCE: 30562.505W0
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: PCT/AU97/00540
PRIOR FILING DATE: 1997-08-23
PRIOR PLILING DATE: 1996-08-23
PRIOR FILING DATE: 1996-08-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 WFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTI
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                                                                                                                             Length 344;
                                                                                                                                                           37; Indels
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                                                                                                                         72.6%; Score 1475; DB 4; 77.7%; Pred, No. 6.9e-162;
                                                                                                                                                         30; Mismatches
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 347
                                                                                                                                          Best_Local Similarity 77.7% Matches 275; Conservative
NUMBER OF SEQ ID NOS: 29 SOFTWARE: Patentin Ver.
                            SEQ ID NO 11

. LENGTH: 344

. TYPE: PAT

. ORGANISM: Homo sapiens

US-09-298-886-11
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; ORGANISM: Lepus Sp.
US-09-254-077A-9
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SLPVLHSSTASRVPWONYHLNDMMEERYRHIPAPYVRLTGYPCSWTFYHHLRHEILREFT 173
                                                                                                                                                                                                       FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 SGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASM 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 AGRPAAPS-----GIWTIHPDGRFGNOMGOYATLLALAQLNGRRAFILPAM 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 LRPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --LPMTTQMS---- 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 LAFLLVCALSAFSFLLHLHQDLFRNGLALSLPCLERQPVPAPVAIVCLPVTSPASNASSC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: SANDRIN, MAURO S.
APPLICANT: MCKENZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30662.505W0
CURRENT APPLICANTON NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 LHDHVREEAQAFLRGLRVNGSRPSTFVGVHVRRGDYVRVMPQVWKGVVADRGYLEQALDW
                                                                                                                                                                                                                                                                                                                        TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 373;
                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.5%; Score 1086.5; DB 4, 57.6%; Pred. No. 6.7e-117; tive 51; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---LOPLSEKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCI/AU97/00540 PRIOR FILING DATE: 1997-08-22 PRIOR PLILING DATE: 1997-08-23 PRIOR FILING DATE: 1996-08-23 PRIOR FILING DATE: 1996-08-23 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/09254077A Patent No. 6399758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 LIFVEVT----STIIHLQQRIVK---
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TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES, ON GLYCOPROPEINS,
TITLE OF INVENTION: GLYCOLYPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
UNDBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 P-----QH-PASISGTWTVYPNGRFGNQMGQYATLIALAQLNGRRAFILPAMHAALAP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRFEIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---RIVKLOPLSEKELPMTTOMSSGNTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,246
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.0%; Score 1057.5; DB 1 56.5%; Pred. No. 1.5e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2363-060-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lavalleye, Jean-Paul M. P. REGISTRATION NUMBER: 31,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                           Sequence 6, Application US/08393246
Patent No. 5595900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 20-JUL-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids TOPOLOGY: unvert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 LAHFLIFVFVTSTIIHLQQ-
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                                                                                                                                                                                                                                                                                LOWE, JOHN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-393-246-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC OPERATING SYSTEM:
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Best Local Similarity
Matches 205; Conserv
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                                                                                                                                                                                                                                             GENERAL INFORMATION:
             363 AKP 365
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                        Sequence 6, Application JS/07914281

Patent No. 5324663

GENERAL INFORMATION:

GENERAL INFORMATION:

TILLE OF INVENTION:

TITLE OF INVENTION:

GENERAL STRUCTURES ON GLYCORRATEINS,

TITLE OF INVENTION:

GENERAL STRUCTURES ON GLYCORRATEINS,

TITLE OF INVENTION:

GENERAL OF SEQUENCES:

GORRESPONDENCES:

ADDRESSEE:

ADDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 ROAMDWFRARHEAPVFVVTSNGMEWCKENIDTSOGDVTFAGDGQEAIPWKDFALLTQCNH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 TIMTIGIFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IAN PC compatible
COMPUTER: IAN PC compatible
OPERATING SYSTEM: PC-DOS/AS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/914,281
FILING DATE: 19920720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.0%; Score 1057.5; DB 1
56.5%; Pred. No. 1.5e-113;
iive 46; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
ATTORNEY/AGRNT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31.451
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703)486-2347
TELEFRAX: (703)486-2347
TELEFRAX: (703)486-2347
TELEFRAX: (703)486-2347
SEQUENCE CHARACTERISTICS:
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-07-914-281-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Sim:
Matches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
US-07-914-281-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-
TELECOMMUNICATION INFORMATION:
TELECPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08525058A Patent No. 5770420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
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56.5%;
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-525-058A-6
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-525-058A-6
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LOCATION: 1.365
LOCATION: 1.365
OTHER INFORMATION: /note= "GDP-L-fuçose:beta-D-Galactoside-2-alpha-L-fucosyl
PUBLICATION INFORMATION:
AUTHORS: Larsen, et al.
JOURNAL: Proc. Nat'l Acad. Sci. USA
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295 TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.0%; Score 1057.5; DB 1; Length 365; 56.5%; Pred. No. 1.5e-113;
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                                                                                                                                                                                                                                                                                                                      for Gastro-Intestinal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                        Street, Suite 2800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/273,411
                                                                                                                                                                                                                                                                                 APPLICANT: Falk, Per APPLICANT: Gordon, Jeffrey I. TITLE OF INVENTION: Animal Model TITLE OF INVENTION: Disease NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION UNDBER: 31,284
REPERENCE/DOCKET NUMBER: WU1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
TELEPAX: (404) 815-6508
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                  Sequence 1, Application US/08273411
Patent No. 5625124
GENERAL INFORMATION:
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MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
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Matches 205;
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GENERAL INCOMMATION:
GENERAL INCOMMATION:
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
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                                                                                                                                             117 IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                                                           P-----QH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMHAALAP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                        235 EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH 294
                                                                                                                                                                                                                                                                                       177 KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1057.5; DB 1; Length 365; Pred. No. 1.5e-113;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,058A
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GDP-L-FUCCOSE: BETA-D-GALACTOSIDE
Z-ALPHA-L-FUCCOSTITRANSFERASES, DNA SEQUENCES ENCODING THE
SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
GENCTYPING A PERSON
    4.
                                                                                                                                                    IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                                        PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
                                                                                                                                                                                                                   KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL 234
                                                                                                                                                                                                                                                                                EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH 294
                                                                                                                                                                                                                                                                                                    295 TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWYGIPADLSPLLKA 354
    Gaps
                             ---RIVKLOPLSEKELPMTTQMSSGNTES 56
                                                         LAFILVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
 Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
87;
Mismatches
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APPLICATION NUMBER: US/08/395,800A
FILINO DATE: 28-FEB-1995
CLASSIFICATION: 435
TELECOMMUNICATION: INFORMATION:
TELERIONE: (703) 413-220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08395800A Patent No. 5807732 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LOWE, JOHN B
APPLICANT: LOWE, APPLICANT: LOWE, STRUCHE, STLVIE
APPLICANT: ROUGUIER, STLVIE
APPLICANT: ROUGUIER, STLVIE
APPLICANT: RILLY, ROBERT J
TITLE OF INVENTION: GDF-L-FUCOS
TITLE OF INVENTION: 2-ALPHA-L-F
46;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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amino acid
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Conservative
                             LAHFLIFVFVTSTIIHLQQ
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TOPOLOGY:
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205;
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SEQUENCES ENCODING THE
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APPLICANT: LOWE, JOHN B

APPLICANT: LENDON, GREGORY

APPLICANT: LENDON, GREGORY

APPLICANT: ROUGUIER, SYLVIE

APPLICANT: ROLLY, ROBERT J

TITLE OF INVENTION: GPD-L-FUCOSE: BETA-D-GALACTOSIDE

TITLE OF INVENTION: 2-ALPHA-L-FUCOSYLTRANSPERASES, DNA SEQUENCES ENCODING

TITLE OF INVENTION: GENOTYPING A PERSON

TITLE OF INVENTION: GENOTYPING A PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                  57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
                                                                                                                                                                                                                           117 IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
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                                                                                                              11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC
                                                                                                                                                                                         P-----QH-PASLSGTWTVYPNGRFGNQMGQYAILLALAQLNGRRAFILPAMHAALAP
                                                                                                                                                                                                                                                                                                      177 KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL
                                                                                                                                                                                                                                                                                                                          EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH
                                                                               -- RIVKLOPLSEKELPMTTQMSSGNTES
                                         25;
     Length 365;
                                         87; Indels
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1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
   Score 1057.5; DB 1;
Pred. No. 1.5e-113;
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                                         46; Mismatches
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28-FEB-1995
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TELEFAX: (703) 413-3000
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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 52.0%;
56.5%;
Query Match
Best Local Similarity 56.55
Matches 205; Conservative
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APPLICATION NUMBER: US,
FILING DATE: 28-FEB-19G
CLASSIFICATION: 435
                                                                           12 LAHFLIFVFVTSTIIHLQQ-
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OPERATING SYSTEM:
SOFTWARE: PatentI
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                                                                                            DB 1; Length 365;
                                                                                       Query Match 52.0%; Score 1057.5; DB 1; Length Best Local Similarity 56.5%; Pred. No. 1.5e-113; Matches 205; Conservative 46; Mismatches 87; Indels
; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-395-800A-10
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--RIVKLOPLSEKELPMTTQMSSGNTES 56 12 LAHFLIFVFVTSTIIHLQQ--

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177 KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL 234

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295 TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA 354

Search completed: May 27, 2003, 15:11:50 Job time: 17.6237 secs

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Sequence 11, Appl
Sequence 10, Appl
Sequence 0, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 13, Appli
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Appl
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                                                                                                                                                                                                                                                                                                                                                                                                             1 MASAQVPFSFPLAHFLIFVF.....RSHFHLKAKGVTCYVAGRAF 380
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Sequence 10
Sequence 2,
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/ cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
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5.1.4_p5_4578
Compugen Ltd.
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US-10-040-863-8

US-10-999-672-110

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US-09-051-034A-2

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US-09-09-672-11

US-10-040-863-11
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US-09-051-034A-4
US-09-844-268-13
US-09-844-705-13
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US-10-214-524-25
US-09-479-614-29
US-09-764-868-647
US-09-815-379-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-848-838-2
US-09-479-614-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375593 seqs, 99172665 residues
GenCore version
Copyright (c) 1993 - 2003
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Listing first 45 summaries
                                                                                                                                          using sw model
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Match Length
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112:
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| Sequence 17, Appl<br>Sequence 6, Appli<br>Sequence 1, Appli             | Sequence 56, Appl<br>Sequence 11366, A | Sequence 212, App | 212,              | 212, | 212,  | 212, | 212, | 212,              | 212. | 212, | 212, | 212, | 212, | 212,              | 212, |       | 212, | 212, | 212, | 212, |                   | 212,              |  |
|---|--|-------------------|-------------------|------|-------|------|------|-------------------|------|------|------|------|------|-------------------|------|-------|------|------|------|------|-------------------|-------------------|--|
| 9 US-09-815-379-17<br>10 US-09-765-298 <b>A</b> -6<br>9 US-10-235-521-1 |  | US-10-028-072-212 | US-10-121-049-212 |      |       |      |      | US-10-176-921-212 |      |      |      |      |      | US-10-142-419-212 | Ð    | -SD   |      | us-  | us-  | us-  | US-10-123-236-212 | US-10-123-261-212 |  |
| 2058 9<br>217 1<br>738 9  |  | 747 9             | 747 9             |      | 747 9 |      |      |                   |      |      |      |      |      |                   |      | 747 9 |      |      |      |      | 747 9             |                   |  |
|   | 4 4<br>5 5                             | 4.1               | 4.1               | 4.1  | 4.1   | 4.1  | 4.1  | 4.1               | 4.1  | 4.1  | 4.1  | 4.1  | 4.1  | 4.1               | 4.1  | 4.1   | 4.1  | 4.1  | 4.1  | 4.1  | 4.1               | 4.1               |  |
| 89<br>87<br>85.5  | 84.5<br>84.5                           | 83.5              | 83.5              | 83.5 | 83.5  | 83.5 |      |                   |      |      |      |      | 83.5 |                   |      |       | 83.5 |      |      |      | 83.5              | 83.5              |  |
| 20 21 22  | 23                                     | 25                | 26                | 27   | 28    | 62   | 30   | 31                | 32   | 33   | 34   | 32   | 36   | 37                | 38   | 39    | 40   | 41   | 42   | 43   | 44                | 45                |  |
|   |  |                   |                   |      |       |      |      |                   |      |      |      |      |      |                   |      |       |      |      |      |      |                   |                   |  |
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RESULT 1

Sequence 8, Application US/0999672

Sequence 8, Application US/0999672

Patent No. US20020127655A1

GENERAL INFORMATION:

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: US/09/999,672

CURRENT APPLICATION NUMBER: US/09/999,672

CURRENT FILING DATE: 2001-10-31

PRIOR APPLICATION NUMBER: US/09/298,886

PRIOR PRILING DATE: 1999-04-26

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin Ver. 2.0

LENGTH: 380

ALIGNMENTS

; ORGANISM: Rattus norvegicus
US-09-999-672-8
Query Match
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-200;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps

TYPE: PRT

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FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLIQCNHIIMTIG 300
                  TFGIWAAYLAGGDIIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACP 360
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: ETIC H. Holmes et al.
TITLE OF INVENTION: NCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GML-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/10/040,863
CURRENT APPLICATION NUMBER: 09/298,886
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VORE. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVNPNVWKGVVADRGYLEKALDM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWYGIPADLSPLLKALTPACP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 2032; DB 12; Length 380; 100.0%; Pred. No. 1.6e-200; Aritive 0; Mismatches 0; Indels 0;
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Patent No. US20020127655Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                     ; Sequence 8, Application US/10040863; Patent No. US20020137165A1
                                                                                                                            RSHFHLKAKGVTCYVAGRAF 380
                                                                                                                                             361 RSHFHLKAKGVTCYVAGRAF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Rattus norvegicus US-10-040-863-8
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US-09-999-672-10
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APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GAL-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT APPLICATION NUMBER: US/09/298,886
PRIOR APPLICATION DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 327
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TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLICSIDE
TITLE OF INVENTION: GAM-SPECIFIC ALPHAl-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NOWBER: US/10/040,863
CURRENT APPLICATION NUMBER: 2001-11-01
PRIOR APPLICATION NUMBER: 2001-11-01
PRIOR FILLING DATE: 1999-04-23
                                                                                                                                                                                                                                                                                                                                                                                        LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 87
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Pred. No. 1.4e-186;
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                                                                                                                                                                                                                                                                                                     93.3%; Score 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.00
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Patent No. US20020137165A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                            ; ORGANISM: Rattus norvegicus US-09-999-672-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Rattus norvegicus US-10-040-863-10
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                                                                                                                                                                                                                                                                                                                                                   Matches 353;
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LENGTH: 353
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
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                                                                                                   US-09-999-672-11
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208 GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                         GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER
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; Pred. No. 4.5e-146;
28; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MCKENZIE, IAN FAROUHAR CAMPBELL
APPLICANT: SANDRIN, MAURO SERGIO
TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENC
TITLE OF INVENTION: GLYCOSYLTRANSFERASE
FILE REFERENCE: 30562.603WO
CURRENT APPLICATION NUMBER: US/09/051,034A
CURRENT APPLICATION NUMBER: PCT/AU97/00492
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: 60/024,279
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
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US-09-051-034A-2
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                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Best Local Simi
Matches 281;
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LENGTH: 340
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Sequence 11, Application US/0999672

GENERAL INFORMATION:

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: MM.-SPECIFIC ALPHAl-2 FUCOSYLTRANSFERASE AND USES

TITLE OF INVENTION: GM.-SPECIFIC ALPHAl-2 FUCOSYLTRANSFERASE AND USES

TITLE OF INVENTION: GM.-SPECIFIC ALPHAl-2 FUCOSYLTRANSFERASE AND USES

TITLE OF INVENTION: UNMBER: US/09/999,672

CURRENT APPLICATION NUMBER: US/09/999,672

CURRENT FILING DATE: 2001-10-31

PRIOR FILING DATE: 1999-04-26
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Patent No. USZÜCZÜZZÜZJÄTĞA1
GENERAL INFORMATION:
APPLICANT: EXIC H. HOLMES et al.
ITTLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF US/10/040,863
CURRENT APPLICATION NUMBER: US/10/040,863
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/298,886
PRIOR FILING DATE: 199-04-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VET: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR
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12;
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APPLICANT: LOWE, JOHN B.

TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
ON GLYCOPROTEINS,
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
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                                                                                                                                           243 RQAMDWFRARHEAPVEVVTSNGMEWCKENIDTSQGDVTFAGDGQEATPWKDFALLTQCNH 302
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56.5%; Pred. No. 2.7e-100;
iive 46; Mismatches 87;
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REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/863,475A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 07/914,281
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MOLECULE IYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 24-May-2001
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09863475A Patent No. US20020102688A1 GENERAL INFORMATION:
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TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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Best Local Similarity 56.55
Matches 205; Conservative
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STATE: Virginia
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APPLICANT: Clark, A. John
APPLICANT: Clark, A. John
APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
TITLE OF INVENTION: Recombination
FILE REFERENCE: 731/002
CURRENT APPLICATION NUMBER: US/10/105,963
CURRENT FILING DATE: 2002-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 P-----QH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMHAALAP 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
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                                                                                                                                                                                                                                                                        37; Indels
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                                                                                                                                                                                                   72.6%; Score 1475; DB 12; 77.7%; Pred. No. 2.7e-143;
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                                                                                                                                                                                                                                                                 30; Mismatches
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PRIOR FILING DATE: 2001-03-21
WIMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/10105963 Publication No. US20030068818A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                     Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 LAHFLIFVFVTSTIIHLQQ-
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                                                              ; TYPE: PRT; ORGANISM: Homo sapiens
US-10-040-863-11
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; ORGANISM: Homo sapiens
US-10-105-963-10
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US-10-105-963-10
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SEQ ID NO 11
LENGTH: 344
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                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: BOSWORTH, BRAD
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                                                                                           350 VGINADLSPL 359
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Best Local Similarity
Matches 194; Conserv
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US-09-844-268-13
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                                                                                                                                                                                                                                                                                    295 TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA 354
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235 EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH
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                                                                                                                                                              177 KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL
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TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
TITLE OF INVENTION: GLYCOSYLTRANSFERASE
FILE REPERENCE: 3052.605%
CURRENT APPLICATION NUMBER: US/09/051,034A
CURRENT APPLICATION NUMBER: DCT/AU97/00492
PRIOR PILICANION NUMBER: 60/024,279
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: 60/024,279
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-22
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APPLICANT: MCKENZIE, IAN FAROUHAR CAMPBELL
APPLICANT: SANÖRIN, MAURO SERGIO
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Best Local Similarity 62.6%;
Matches 194; Conservative 38
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                                                                                                                                                                                                                                                                                                                                               355 LTP 357
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LENGTH: 365
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TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
TITLE OF INVENTION: RESISTANT TO F18 E. COLI ASSOCIATED DISEASES
FILE REFERENCE: 21419/99368
CURRENT APPLICATION NUMBER: US/09/844,268
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 09/443,766
PRIOR FILING DATE: 1999-11-19
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Patent No. US20020133836A1
GENERAL INFORMATION.
APPLICANT: BOSWORTH BRAD
APPLICANT: VOGELL, PETER
TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
TITLE OF INVENTION: RESISTANT TO F18 E. COLI ASSOCȚATED DISEASES
FILE REPERENCE: 21419/9036 08
CURRENT APPLICATION NUMBER: US/09/844,705
CURRENT FILING DATE: 2001-04-27
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                                  44 PMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRL 103
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70 QHLPKLVRDALKYIGFDRVSQEIVFEYEPKLLKPSRLTYFFGYFQDPRYFDAISSLIKQT 129
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CURRENT FILING DAIE: 2000-01-07
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER FILING DAIE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                      RESULT 14 US-09-479-614-14 Sequence 14, Application US/09479614; Publication No. US20030013183A1; GENERAL INFORMATION:
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Best Local Similarity 20.6'
Matches 89; Conservative
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ORGANISM: Felis catus
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US-09-479-614-14
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                                                                                                                                                                                                                         104 AFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPC 163
                                                                                                                                                                                                                                                                                                                                                                                                   PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                            221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TLFALARMNGRLAFIPASMHNALAPIFRIS-- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMP
                                                                                                                                                                                                                                                                                                                                         222 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS
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                                                                                                                                                   DB 10; Length 365;
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                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                               51.4%; Score 1044.5; DB 10;
62.6%; Pred. No. 5.8e-99;
Live 38; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Taylor, Diane
APPLICANT: Taylor, Diane
APPLICANT: Wang, Ge
APPLICANT: Palcic, Monica
ITILE OF INVENTION: ALF4A 1.2-FUCOSYLTRANSFERASE
FILE REFERENCE: 07254-061002
CURRENT APPLICATION NUMBER: US/09/848,838
CURRENT APPLICATION NUMBER: US 09/433,598
PRIOR PILING DATE: 1999-11-02
PRIOR APPLICATION NUMBER: US 60/107,268
PRIOR APPLICATION NUMBER: US 60/107,268
PRIOR APPLICATION NUMBER: US 60/107,268
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.9%; Score 141; DB 10;
24.0%; Pred. No. 3.8e-06;
tive 33; Mismatches 125;
PRIOR APPLICATION NUMBER: 09/443,766
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 13
SOFINARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09848838
Patent No. US200220037570A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Helicobacter pylori
US-09-848-838-2
                                                                                                                                                            Best Local Similality ... Matches 194; Conservative
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Best Local Similarity 24.0°
Matches 81; Conservative
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                                                                                   ; TYPE: PRT
; ORGANISM: Porcine
US-09-844-705-13
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US-09-848-838-2
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LENGIH: 300
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APPLICANT: Weber, Eric
AITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1087
179 FTL-----HDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 229
                                                                                                                                                                                                                                                      226 DKBEEAYWDMLLMQSCKHGIIANSTYSWWAAYL-----MEN---PEKIIIGPKHWLFG 275
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                                     230 DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFA--.
                                                                                                                                                          180 GIDYQKKALEYMAKRVPNMELFV-----FCE------DLKFTQNLDLGYPFTDMTTR
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; Pred. No. 0.005;
40; Mismatches 127; Indels 176;
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328 VFLPPEGEPKTK 339

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US-09-479-614-2
Sequence 2, Application US/09479614
Publication No. US20030013183A1
Sequence 1. Worker 2. US20030013183A1
Septence 2. Application US/09479614
Publication No. US20030013183A1
APPLICANT: McCall, Catherine
APPLICANT: Weber, Fric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REPRENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: 66/115,033
EARLIER APPLICATION NUMBER: 1999-01-07
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 -TEPATLOETSGLYTTTSHVTVSGEWAKQKFTCSVAHAESPTINKTVSACTMNFIPPTVK 180
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5.6%; Score 113; DB 9; Length 496;
Best Local Similarity 20.6%; Pred. No. 0.0061;
Matches 89; Conservative 40; Mismatches 127; Indels 176;
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Search completed: May 27, 2003, 15:25:41 Job time : 19.4181 secs

342 VGIPADLSPLLK 353 | :| : | ·| 393 VFLPPEGEPKTK 404

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                                                                                                          1 MASAQVPFSFPLAHFLIFVF.....RSHFHLKAKGVTCYVAGRAF
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                     283224 seqs, 96134422 residues
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Listing first 45 summaries
                                    protein search, using sw model
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B56392
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Gapop 10.0 , Gapext 0.5
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                                                     May 27, 2003, 15:00:45
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R; Kelly, R.J.; Rouquier, S.; Glorgi, D.; Lennon, G.G.; Lowe, J.B.
J. Biol. Chem. 270, 4640-4649, 1995
A; Title: Sequence and expression of a candidate for the human Secretor blood tes with the non-Secretor phenotype.
A; Reference number: A56098; MUID:95181460; PMID:7876235
A; Accession: A56098
                                                                      probable membrane
                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 03-Oct_1995 #sequence_revision 03-Oct-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
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A; Molecule type: DNA
A; Residues: 1-343 <KEL>
A; Cross-references: GB:U17894; NID:g687618; PIDN:AAC24453.1; PID:g687619
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:120619; OMIM:182100
A;Map position: 19q13.3-19q13.3
C;Keywords: qlycoprotein; Golgi apparatus; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.1%; Score 1485.5; DB 2; Lengtl 77.9%; Pred. No. 2.5e-116; ive 30; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                   alpha(1,2)fucosyltransferase Sec2, long form - human
                                                                                                                                                                                                                                                              ALIGNMENTS
T19293
T04452
E85384
VGBEEA
JN0920
S61964
AB2934
                                                                                                E98348
A59267
VGBEG3
A54688
T45082
T08679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 77.9
Matches 275; Conservative
 A; Gene: GDB: FUT2; SE
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us-10-040-863-8.rpr

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C;Accession: A36047
R;Larsen, R.D.; Ernst, L.K.; Nair, R.P.; Lowe, J.B.
R;Larsen, R.D.; Ernst, L.K.; Nair, R.P.; Lowe, J.B.
A;Litle: Acad. Sci. U.S.A. 87, 6674-6678, 1990
A;Title: Molecular cloning, sequence, and expression cf a human GDP-L-fucose;beta-D-g
A;Reference number: A36047; MUID:90370848; PMID:2118655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superiors: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 10-Sep-1997
                                    A;Cross-references: GB:M35531; NID:g183887; PID:g306830
C;Kcywords: glycosyltransferase; hexosyltransferase; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHH 170
                                                                                                                                                                                               229 ADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFAL 288
                                                                                                                                                                                                                                                                                           LTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMENALAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIMTIGIFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKALDMFRARYSSPVFVVISNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 ROAMDWFRARHEAPVFVVTSNGMEWCKENIDTSOGDVTFAGDGOEATPWKDFALLTOCNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.0%; Score 1057.5; DB 2; Length 365; illarity 56.5%; Pred. No. 1.5e-80; Conservative 46; Mismatches 87; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 LAHFLIFVFVTSTIIHLQQ---
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-365 < LAR>
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                                                                                                                                                                                                                                                                                                                                                                                   SPL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                 SPV 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365
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beta-galactoside alphal,2-fucosyltransferase II - rabbit
C;Species: Oyrochagus cuniculus (domestic rabbit)
C;Species: Oyrochagus cuniculus (domestic rabbit)
C;Accession: B56392
E;Ritocshi, S.; Kaunocki, S.; Kanazawa, I.; Tsuji, S.
J. Biol. Chem. 270, 8844-8850, 1995
A;Title: Molecular cloning and expression of two types of rabbit beta-galactoside alphal
A;Reference number: A56392; MUID:95238380; PMID:7721792
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deta-galactoside alphal, 2-fucosyltransferase I - rabbit C;Species: Orycrolagus cuniculus (domestic rabbit) C;Species: Orycrolagus cuniculus (domestic rabbit) C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999 C;Accession: A55392 Rsquence_revision 19-Oct-1995 #text_change 05-Nov-1999 R;Hitoshi, S:; Kusunoki, S.; Kanazawa, I.; Tsuji, S. A;Hitoshi, S:; Kusunoki, S.; Kanazawa, I.; Tsuji, S. A;Hitoshi, S:; Kasunoki, S:; Kusunoki, S:; Kanazawa, I.; Tsuji, S. A;Hitoshi, S:; Kasunoki, S:; Wulb:95238830, PMID:7721792 A;Accession: A55392
                                                                                                                                                                                                                                                                                                                                                                                                         5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASM 110
                                                                                                                                                                                                                                                                                                                                                                                                                                             14 HFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-373 <HIT>
A; Residues: 1-373 <HIT>
A; Cross-references: GB:X80226; NID:g854354; PIDN:CAA56513.1; PID:g854355
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-354 <HIT>
A:Cross-references: GB:X80225; NID:9854356; PIDN:CAA56512.1; PID:g854357
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 MFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAFLIVCALSAFSFLLHLHQDLFRNGLALSLPCLERQPVPAPVAIVCLPVTSPASNASSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 YFLFIIFVVSTVFHCHORLAL------VPAPWAYSARVVVVP------GHLPREĞ
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                                                                                                                                                                                                                                                                                                                                                           Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 373;
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                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                   64.9%; Score 1319.5; DB 2; 73.2%; Pred. No. 1.9e-102; 1ive 27; Mismatches 47; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.5%; Score 1086.5; DB 2; 57.6%; Pred. No. 5.7e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 TIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIFVFVT----STIIHLQQRIVK-----LQPLSEKE---
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                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 248; Conserv
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Best Local Similarity
Matches 209; Conserv
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hypothetical protein wbla [imported] - Vibrio cholerae C.Species: Vibrio cholerae C.Species: Vibrio cholerae [C.Species: Vibrio [C.Species: Vibrio [C.Species: Vibrio [C.Species: Vibrio [C.Species: Vibrio [C.Species [C.Species: Vibrio [C.Species
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Science 282, 2012-2018, 1998
A.Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A: Mitle: Genome sequence of the nematode C. elegans: a platform for investigating bio A: Reference number: A75000; MUID: 99609613; pMID: 9851916
A: Note: see Websites genome. wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A: Molecule type: DNA
A: Residues: 1-443 <STO>
A: Residues: 1-443 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein B0205.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H8/911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 MFTINSIGRLGNQMGEYATLFALARMNG---RL---AFIPASMHNALAPIFRISLPVLHS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----NDWMEERYRHI-----PGHFVRFT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 GYPCSWIFYHHLRPBILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 MPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 GSPAKDFALLTQCNHTIMTIGTFGIWAAYL-AGGDTIYLANYT------LPDS 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: wbla
C;Superfamily: Vibrio cholerae hypothetical protein wbla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.6%; Score 214.5; DB 2; llarity 26.5%; Pred. No. 2.5e-10; Conservative 50; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 183; DB 2;
Pred. No. 1.9e-07;
      9.0%;
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Best Local Similarity
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Best Local Simi
Matches 79;
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                                  121
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Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) B - rat (fragment)
N;Alternate names: alpha-1,2-fucosyltransferase
N;Alternate names: alpha-1,2-fucosyltransferase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Dec-1994 #sequence_revision 23-Feb-1996 #text_change 08-Oct-1999
C;Accession: S46494
B;Plau, J.P.; Labbarriere, N; Dabouis, G; Denis, M.G.
Biochem. J. 300, 623-626, 1994
A;Title: Evidence for two distinct alpha-(1,2)-fucosyltransferase genes differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Cross-references: EMBL:L26009; NID:9414814; PIDN:AAB41514.1; PID:9554438
R)Plau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
Biochem. J. 300, 623-626, 1994
A:Title: Evidence for two distinct alpha-(1,2)-fucosyltransferase genes differentially A)Reference number: $46493; MUID:94280382; PMID:8010942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ć
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Dacte: 07-May-1995 #sequence_revision 17-Nov-1995 #text_change 08-Oct-1999
C;Accession: S51582; S46493
R;Piau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
submitted to the EMBL Data Library, November 1993
A;Reference number: S51582
                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-159 <PIA>
A;Cross-references: EMBL:L26010; NID:g414815; PIDN:AAB41515.1; PID:g414817
C;Genetics:
A;Gene: FTB
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 PCSWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVN--GSQPSTFVGVHVRRGDYVHV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 MPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPNRWKGVVGDRAYLQXAMDWFRARHKDPIFVVTSNGMRWCLENIDISHGDVVFAGNGGE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 846; DB 2; Length 15
Pred. No. 2.3e-63;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 VGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 581; DB 2;
Pred. No. 2.6e-41;
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A;Molecule type: mRNA
A;Residues: 9-135 <P12>
A;Cross-references: EMB;:L26009
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
28.6%; Score 581; DB
Best Local Similarity 73,2%; Pred. No. 2.6e
Matches 104; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 GSPAKDFALLTQCNHTIMTIGT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 99.4
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-159 <PIA>
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A;Molecule type: mRNA
A;Residues: 1-142 <PIA>
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Gaps

Length 281;

334 EFISEDYYLPHW 345

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| Watches 72; Conservative 5 19 1GNOMGENATIFALARMNGRIAF 19 103 IGNIAMFQVAGILISIARETGSILL 0y 134 |
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hypothetical protein C17A2.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Oacurothabditis elegans
C;Accession: T31316
R;Sammons, L.; Wohldmann, P.
Submitted to the EWBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C17A2.
A;Reference number: Z21098
A;Accession: T31916
A;Accession: T31916
A;Accession: T31916
A;Accession: T318 cSAM>
A;Residues: J348 cSAM>
A;Cross references: EMBL:AF016654: PIDN:AAB66030.1; GSPDB:GN00020; CESP:C17A2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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A;Experimental source: strain Bristol N2; clone K06H6
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein K06H6.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct_1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 LRGMFTINSIGRLGNQMGEYATLFALARMNGR--LAFIPASMHNALAPIFRISLP---- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 RPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGV-VAD 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 --VLHSDTAKKI---PWQ----NYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 RGYLEKALDMFRARYSSPV-----FVVTSNGMAWCR---EN--INASRGDVVFAGNG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 PDFIRNSVKYIAENFIPEIEYKKVHRKVVIFGDDLEFMRSLFENSVVSTDEPEYMFPAEY 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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6 VVHSKMFRVPXVLHFNS------TEHFLSSNLASP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 ------SRLGNHIFFEFASLFGLSERLHRTPLFLVENEFHQKMLDETRKVMPGLVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 2
A;Introns: 94/3; 133/3; 168/2; 272/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.7%; Score 156.5; DB 2; Length 348; 20.9%; Pred. No. 2.3e-05; tive 57; Mismatches 118; Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 I--EGSPAKDFALLTQ-CNHTIMTI--GTFGIWAAYLAGGDTIY 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 YISQNSPAEDLIYSKQNCDIVLISAPKSTFGWWIGXFSKGNKVF 291
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R)David, M.; Wohldmann, P.; Bauer, C.; Clarke, K.
submitted to the BNBL Data Library, September 1997
A; Bescription: The sequence of C. elegans cosmid K06H6.
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A;Status: prealiminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-335 <DAV>
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Best Local Similarity 20.9%
Matches 72; Conservative
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A; Gene: CESP:C17A2.4
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| QY 223 VWKGVVADRGYLEKALDMFRARYSSPVFVVT  DD 226 RPSDATFTRAATDFLVDLXRKSHERVNVVVV  QY 283 AKDFALLTQ  DD 272 AHFTFLQKPVNNSYDYSLPQISPSYTAILTP  QY 305 WAAYLAGGD-TIYLANYTLPDSPFLKVFKPE  DD 332 WLSYLAKRTATTYYRDILESKDGVAGEWHPE  | RESULT 13 T22068 hypotherical protein F41D3.6 - Caenorhabd C, Species: Caenorhabditis elegans C, Date: 15-Oct-1999 #sequence_revision 15 C, Accession: T22068 R,White, S. Submitted to the EMBL Data Library, Novem A, Reference number: 219508 A, Accession: T22068 A, Status: preliminary: translated from GBA, Status: preliminary: translated from GBA, Residues: 1-50 cMILL A, Residues: 1-50 cMILL A, Cross references: EMBL: 81537; PIDN: CABBA, Comential source: clone F41D3 C, Genetics: A, Map position: 1 |  | OY 285 DFALLTOCNHTIMIT-  DD 249 DIRIMKTLMEDAIDDLHFSQIYCDSVLITAR  OY 326 PFLKVFKPEAAFLPEW 341    ::     :     :    DD 309 VQLQWTK-EDFYPPTW 323  RESULT 14  H71976  probable alpha(1,2)fucosyltransferase - HC; Species: Helicobacter pylori C; Species: Helicobacter pylori A; Variety: Strain J99 C; Date: 12-Feb-1999 #sequence_revision 12 C; Cate: 12-Feb-1990 #sequenc |
|---|---|--|---|
| A; Map position: 5 A; Introns: 1771; 32/2; 58/1; 111/3; 150/3; 184/2; 218/1; 243/3; 272/1; 303/3 C; Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3 Query Match Best Local Similarity 22.8%; Pred. No. 3.9e-05; Matches 77; Conservative 50; Mismatches 118; Indels 93; Gaps 19; QY 51 SGNTESPEMREDSEQHGNGELRGMFTINSIGREGNOMGENATLFALARMNGRLA-FIPA 108 | CVEVDPLIHEHNNDE  LRGLEVNGSQP    :   | PRESULT 12 T20572 hypothetical protein F08A8.5 - Caenorhabditis elegans C;Species: Tabort-1999 #sequence_revision 15-oct-1999 #text_change 20-Jun-2000 C;Accession: T20572 R;Harris, B. Submitted to the EMBL Data Library, October 1997 A;Reference number: 219294 A;Reference number: 219294 A;Reference number: 219294 A;Reference number: 219294 A;Reference number: J20572 A;Molecule type: DNA A;Residues: 1-383 <wil> A;Residues: 1-383 <wil> A;Residues: 1-383 <wil> A;Residues: Clone F08A8 A;Residues: Caence: clone F08A8 A;Reperimental source: clone F08A8 C;Genetics: A;Map position: 1 A;Introns: 16/1; 51/3; 77/1; 131/3; 170/3; 209/2; 244/1; 269/1; 297/3; 324/1; 354/3 C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3</wil></wil></wil> | Query Match Best Local Similarity 21.4%; Score 146; DB 2; Length 383; Batches 87; Conservative 55; Mismatches 148; Indels 116; Gaps 16;  Qy 13 AHFLIEVFUSTIIHLQQRIVKLQPLSEKELPMITQMSSGNTESPEMRRDSEQHGNGELR 72   |

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King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D. lls, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
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No. 0.0012;
smatches 105; Indels 89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| : |: |: |: IA-----VFNSSDPVLQSNLEFLNQKLPRIS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THINDWMEERYRHIPGHFURFTGYPCSWTFY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNGSQPSTFVGVHVRRGDYV----HVMPNVW 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNGMAWCRENINASRGDVVFAGNGIEGSPAK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSNGMAWCRENINASRGDVVFAGNGIEGSP 282
                  Q-----GNHTIMII--GTFGI 304
                                                                         Helicobacter pylori (strain J99)
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                                                                                                                                                                                                                                                                                          ember 1996
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| A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path<br>A;Reference number: A71800; MUID:99120557; PMID:9923682  | QY     |
|--|--------|
| A.Status: preliminary<br>A.Molecule type: DNA<br>A.Residuss: 1-299 <arn><br/>A.Cross-references: GB:AE001447; GB:AE001439; NID:g4154583; PIDN:AAD05659.1; PID:g415458<br/>A.Pynerimental source: ctrain 199</arn>              | 40 QV  |
| C;Ganetics:<br>A;Gene: jhp0086<br>C;Superfamily: Vibrio cholerae hypothetical protein wblA   | oy     |
| Query Match 6.6%; Score 133.5; DB 2; Length 299; Best Local Similarity 22.9%; Pred. No. 0.0016; Matches 76; Conservative 38; Mismatches 129; Indels 89; Gaps 13;   | Search |
| QY 81 GRLGNQMGEYATLFALARWNGRLAFIPASMHNALAPIFRIS 121  | 2000   |
| QY 122 :-LPVLHSDTAKKIPWQNYHLNDWMEBRYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKE 178  |        |
| QY 179 FTLHDHVREEAQAFLRGLR-VNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRG 232   |        |
| QY 233 YLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFA 287   |        |
| QY 288LLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAF 337   |        |
| QY 338 LPEWVGIPADLSPLIKALTPACPRSHFHLKAK 369  |        |
| RESULT 15  |        |
| T25309 hypothetical protein T26E4.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000 C;Accesion: 75309 |        |
| R.MCNULSSION. 12235.<br>R.MCNULSY, A. submitted to the EMBL Data Library, October 1996<br>A.Reference number: 220013   |        |
| A;Accession: T25309<br>A;Status: preliminary; translated from GB/EMBL/DDBJ<br>A;Molecule type: DNA   |        |
| A;Residues: 1-365 <wil> A;Cross-references: EMBL:281132; PIDN:CAB03434.1; GSPDB:GN00023; CESP:T26E4.4 A;Experimental source: clone T26E4</wil>   |        |
| C;Genetics:<br>A;Gene: CSE9:T26E4.4<br>A;Map position: 5<br>A;Introns: 50/1; 80/2; 140/3; 179/3; 218/2; 253/1; 278/1; 306/3; 325/1; 342/3<br>C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3                |        |
|  |        |
| QY 84 GNOMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDIAKKIPWQ 136  |        |
| QY 137 NYHLNDWMEERYRHIPGHFVRFTGXPCSWTFYHHLRPEILKEFT 180 :   :   :             b 143 SVSSHQMNWVKCIFDDPKKMLNRSEQHLMLNGHYFQSFKYFHHLRSEIREWLA 196  |        |

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| Qy | 181 | 181 LHDHYREEAQAFLRGLRYNGSQPSTFYGYHYRRGDYVHYMPNYWKGYVADRGYLEK 236      |  |
|----|-----|---|--|
| Db | 197 | 197 PSKMAKLAAETVLTSELKEDLIICTHIRRGDFQTDGVH-QPSDPNFTRA 244             |  |
| οy | 237 | 237 ALDMFRARYSSPVFVVTSNGMAWCRENI                                      |  |
| qq | 245 | 245 AIDFLVKHYQKWHYRITYVVVPGNDVNESKAVFEDRVSNSSVIPNRITPPLNFPIPENSPK 304 |  |
| QY | 269 | 269 GDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAXLAGGDTIYLANYIL 322        |  |
| qq | 305 | 305 YSVILPQNSTPENDLAFSRQAPSSTFGWWLSYLAKKSAVYLRPFCL 350                |  |

completed: May 27, 2003, 15:08:15

OM protein - protein search, using sw model

Run on:

May 27, 2003, 14:53:11; Search time 11.122 Seconds (without alignments) 1417.108 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-040-863-8 2032 1 MASAQVPFSFPLAHFLIFVF......RSHFHLKAKGVTCYVAGRAF 380

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues

Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100% '
Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARTES

|           | scriptio       | 518 | h dalac    | bos taurus | Sum        | orvo       |            | Q10980 rattus norv | orvet | P19526 homo sapien | sns      | rattı    | caenor     |            | porphyr    |           |               |          | equine     | equine     | mus mus    | homo       | Q56222 thermus the | P15325 emericella | Q13370 homo sapien |            | ratt    | heli       |           | mycobac    |            | шае       | 03934 caenorhabd | orphyromo  |  |
|-----------|----------------|-----|------------|------------|------------|------------|------------|--------------------|-------|--------------------|----------|----------|------------|------------|------------|-----------|---------------|----------|------------|------------|------------|------------|--------------------|-------------------|--------------------|------------|---------|------------|-----------|------------|------------|-----------|------------------|------------|--|
| SUMMARIES |                |     | FUT2_HUMAN | FUT2_BOVIN | FUT2_MOUSE | FUT2_RABIT | FUT1_MOUSE | FUT1_RAT           | - 1   | FUT1_HUMAN         | FUT1_PIG | FUT2_RAT | YKQ7_CAEEL | VGLD_HSVEK | FMA3_PORGI | CDH_PHACH | MY10_HUMAN    | PTN7_RAT | VGLD_HSVEA | VGLD_HSVEB | GRB2_MOUSE | GRB2_HUMAN | NQO1_THETH         | OUTD_EMENI        | CN3B_HUMAN         | PLO3_HUMAN | LPH_RAT | RIBB_HELPY | AAT_THEAQ | CTPC_MYCTU | A4B1_MOUSE | POLG_MVEV | TC1A_CAEEL       | FMB2_PORGI |  |
|           | DB             |     | Н          | Н          | Н          | Н          | Н          | <b>,</b> —i        | Н     | ٦                  | ~1       | Н        | -1         | ~          | Н          | -1        | <del></del> i |          | Н          | Н          | ~          | П          | Н                  | -                 | Н                  | -          |         | ~          | ٦         | Н          | Н          | Н         | Н                | М          |  |
|           | Length         | 34( | 343        | 344        | 368        | 354        | 376        | 376                | 373   | 365                | 365      | 159      | 365        | 442        | 353        | 77        | 2058          | 359      | 402        | 452        | 217        | 217        | 438                | 23                | 1112               | 73         | 1928    | 344        | 383       | 718        | 73         | 1780      | 273              | 350        |  |
| 99        | Query<br>Match | 73  | ص          | 'n         | 7.         | 4.         | 4          | ₹.                 | ë.    | 52.0               | .i.      |          |            | ٠          | ٠          | •         | •             | •        | ٠          | 4.4        | 4.3        | 4.3        | 4.3                | 4.3               | 4.3                | 4.2        | ٠       | •          | 4.2       | 4.2        |            |           | 4.1              | 4.1        |  |
|           | Score          | Н   | ഗ          | 7          | ന          | 318        | $\vdash$   | H,                 | 980   | 1057.5             | 020      | 846      | 168        | 16         | 5 B        | 89        |               | œ        | 88.2       | $\infty$   | 88         | 87         | 18                 | ١.                | φı                 | 85.5       | so.     | 4.         | ず         | 4          | 84         |           | 83.5             | m          |  |
|           | Result<br>No.  | Н   | 7          | m          | 4          | S          | 9          | 7                  | α0 -  | σ,                 | ) T      | <b></b>  | 7.         | . T        | ΨŢ,        | 15        | 10            | 17       | 18         | 19         | 20         | 271        | 77                 | 2.43              | 4.1                | 220        | 20      | 7.7        | 87        | 58         | 30         | 31        | 32               | ო<br>ო     |  |

| P05418 paracoccus Q61409 mus musculu P76464 escherichia P45784 vibrio chol P72933 synechocyst P87503 human adeno P97846 rattus norv P7837 homo sapien P87379 xenopus lae Q92140 helicobacte P14014 bacillus li P23739 rattus norv |  |
|---|--|
| CYB_PARDE CN3B_MOUSE CN3B_MOUSE GSPN_UDCH GSO_SYNX3 DPOL_ADE04 CTA1_AAT CTA1_HUMAN GRB2_XENLA GRB2_XENLA GRB2_XENLA GUST_BACLI SUIS_RAT   |  |
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| 440<br>799<br>1534<br>252<br>257<br>1193<br>1381<br>1384<br>217<br>314<br>718   |  |
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## ALIGNMENTS

| CELCHMENTS | SULT 1<br>12_PIG<br>FUT2_PIG<br>Q10982; Q290 | DE D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)<br>DE (Fucosyltransferase 2).<br>GN FUT2. | <br>KN 11.<br>RP SEQUENCE FROM N.A.<br>RX MEDLINE-97468270; PubMed-9321466;<br>RA Meijerink E., Fries R., Voegeli P., Masabanda J., Wigger G., | RP SEQUENCE FROM N.A.  RA CODNEY S., Mouhtouris E., McKenzie I.F.C., Sandrin M.S.;  RT "Molecular cloning and characterization of the pig secretor type of the pig secretor |      | <pre>J. Biol. Chem. 270:26577-: -!- CATALYTIC ACTIVITY: GI alpha-L-fucosyl-1,2-be -!- PATHWAY: Glvcosylation</pre> | C -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND C FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY) | ເ ທ ≽ | or send |
|------------|--|---|--|--|------|--|---|-------|---------|
|            |  | <br>0   | <br>   | <br>   | <br> | <br>_ 000  | 700   |       | ر       |

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CARBOHYD
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JWA-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (BC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
(Fucosyltransferase 2) (Secretor blood group alpha-2-fucosyltransferase) (Secretor factor) (Se) (SE2).
                                                                                       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                     61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                      181 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM 240
                                                                                                                                                                                                                                                                                                                                                                                             241 FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
                                                                                                                                                                                                                                                                                                                                                                                                         73.9%; Score 1502; DB 1; Length 340;
79.6%; Pred. No. 1.3e-119;
Live 28; Mismatches 30; Indels 14; Gaps
                                                                                                                                                                                                                                 1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95181460; PubMed=7876235; Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.; Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.; Sequence and expression of a candidate for the human Secretor blood group alpha(1,2)fucosyltransferase gene (FUT2). Homozygosity for an enzyme-inactivating nonsense mutation commonly correlates with the non-secretor phenotype.";
                                                                                                           LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

R -> H (IN REF. 3).

W-> H (IN REF. 3).
                                                                                                                                                                                                                                                                                                              121 SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT
                                                                                                                                                                                                                                                                                                                                                               1 MLSMQASFFFPTGPFILFVFTASTIFHLQQRMVKIQP--TWELQMVTQVT---TESP---
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
      EMBL; U70881; AAB81883.1; -.
EMBL; XF027304; AAC09170.1; -.
EMBL; X99621; CAA67932.1; -.
InterPro; IPR002515; GT_11.
Pfam; PF01531; G1yco_transf_11; 1.
Pransferase; G1ycosyltransferase; G1ycoprotein; Transmembrane; G01gi stack; Signal-anchor. CYTOPLASMIC (POTENTIAL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                301 TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                           Best Local Similarity /9.00
Matches 281; Conservative
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340 AA;
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Q10981;
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Best Local
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FUT2 OR 9
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LIMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. '..) (POTENTIAL).
N-LINKED (GLCNAC. '..) (POTENTIAL).
I -> V (IN XHOSA POPULATION).
/FIId=VAR_003422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Extensive polymorphism of the FUT2 gene in an African (Xhosa)
population of South Africa.";

Hum. Genet. 103:204-210(1998).

-1- FUNCTION: CREATES A SQLUBLE PRECURSOR OLIGOSACCHARIDE FUC-ALPHA
((1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN ESSENTIAL
SUBSTRATE FOR THE FINAL STEP IN THE SQLUBLE A AND B ANTIGEN
SYNTHESIS PATHWAY. H AND SE ENZYMES FUCOSYLATE THE SAME ACCEPTOR
SUBSTRATES BOT EXHIBIT DIFFERENT KN VALUES.
-- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
--- PATHWAY: GlyCOSYLAION.
--- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
--- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
--- STEMBNANTURE DOCUMENT AND SECOND AND STEMBLE OF GOLG.
SEQUENCE FROM N.A., AND VARIANT PHE-140.
SEQUENCE FROM N.A., AND VARIANT PHE-140.
Kudo T., Iwasaki H., Nishihara S., Shinya N., Ando T., Narimatsu I.,
Narimatsu H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY THE USE OF
ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-!- TISSUE SPECIFICITY: SMALL INTESTINE, CÓLON AND LUNG.
-!- MISCELLANBOUGS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE
GALACTOSIDE 2-L-POCOSYLIRANSFERASE THEY ARE EXPRESSED IN A
TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF
MESODERNAL OR ENDODERNAL ORIGIN RESPECTIVELY.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLIRANSFERASE FAMILY 11.
                                                                                                                                                                  "Molecular genetic analysis of the human Lewis histo-blood group
system. It. Secretor gene inactivation by a novel single missense
mutation A385T in Japanese nonsecretor individuals.";
J. Biol. Chem. 271:9830-9837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T., du Toit B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
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Pfam: PF01531; Glyco_transf_11; 1.

Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack; Alternative initiation; Blood group antigen; Polymorphism.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND VARLANT PHE-140.
MEDLINE=97363210; PubMed=9219535;
Koda Y., Soejima M., Wang B., Kimura H.;
"Structure and expression of the gene encoding secretor-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           galactoside 2-alpha-L-fucosyltransferase (FUT2).";
Eur. J. Biochem. 246:750-755(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu Y., Koda Y., Soejima M., Pang H., Schlaphoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LONG ISOFORM.
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MEDLINE-98431007; PubMed-9760207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, U17894, AAC24453.1, -.
EMBL, D89327, BAA13944.1, -.
EMBL, D87942, BAA21684.1, -.
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InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             galactoside 2-alpha-L-Fucosyltransferase.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                             44;
                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
                                                                                                                                                                                                                                           27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Gastrointestinal tract;
                                                                                                                                                                                                              72.1%; Score 1466; 77.1%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                        344 L189 N-255 N-283 N-309 N-39320 MW;
                                               Signal-anchor.
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                 344 AA;
                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 272; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                          29
189
255
309
                                                 Golgi stack;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUT2 OR SEC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ICR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUT2_MOUSE
P97353;
                                                                              LRANSMEM
                                                                                                                        CARBOHYD
                                                                                                                                       CARBOHYD
                                                                                                                                                     CARBOHYD
                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                 SEQUENCE
                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUT2_MOUSE
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KW
FT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GDP-L-fucose:beta-
                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                  121 SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
                                                                                                                                                                                                                                                                                                                                              169
                                                                                                                                                                 Gaps
                                                                                                                                                                                          1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVXLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN, MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                              LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI
                                                                                                                                                                                                                                                                                                                                                                                      FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHIIMTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petit J.M.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
-!- PATHWAY: Glycosylation.
                                                                                                                                                                 11;
                                                                                                                                 Score 1485.5; DB 1; Length 343; Pred. No. 3.4e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 353
                             -> F (IN JAPANESE SEJ ALLELE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 14, Last annotation update)
2-Licosyltransferase 2 (EC 2.4.1.69) (GDP-L-fu
de 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C (IN XHOSA POPULATION).
                                                         /FTId=VAR_003424.
D -> N (IN XHOSA POPULATION)
/FTId=VAR_003425.
                                                                                                                                                                37; Indels
                                                                                                     12066D9CF175E13A CRC64;
             /FTId=VAR_003423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
                                                                                                                                                              30; Mismatches
                                           SECRETOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                     39017 MW;
                                                                                                                                  73.18;
77.98;
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                                                                                                                                                              Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                           140
                                                                        172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Fucosyltransferase 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae; Bos
NCBI_TaxID=9913;
                                                                                                    343 AA;
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                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                     172
138
                           140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D-galactoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (
15-JUN-2002 (
Galactoside 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUT2_BOVIN
Q28113;
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"Molecular cloning and expression of a GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase in murine gastrointestinal tract."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:Deta-D-galactoside 2-lapha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
(Fucosyltransferase 2) (FUT-III). CYTOPLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) 51 TPSRPQPRPQLKGMWIINAIGRLGNQMGEYATLYALAKMNGRAAFIPPQMHSTLAPIFRI 110 180 181 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM 240 61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120 241 FRARYSSPVFVVISNGMANCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300 Gaps 1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60 Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S., "Molecular cloning and expression of a mouse GDP- $\mu$ -fucose: beta-D-121 SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus (GLCNAC. .) (POIENTIAL). (GLCNAC. .) (POIENTIAL). (GLCNAC. .) (POIENTIAL). (GLCNAC. .) (POIENTIAL). 10; Length 344; (POTENTIAL). LUMENAL, CATALYTIC (POTENTIAL) Lin B., Hayashi Y., Saito M., Sakakihara Y., Yanagisawa M., Iwamori M.; 291 TFGIWAAYLAGGETIXLANYTLPDSPELKIFKPEAAFLPKWIGIPADLSPLLK TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK Indels N-LINKED (GLCNAC. .) (POI N-LINKED (GLCNAC. .) (POT N-LINKED (GLCNAC. .) (POT N-LINKED (GLCNAC. .) (POT N-LINKED (GLCNAC. .) (POT N-LINKED (GLCNAC. .) (POT

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                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ώ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 PLAHFLIF--VFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGN 68
CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
PATHMAY: Glycosylation:
SUBCELLGLAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
MISCELLANEOUS: THERE ARE INO GENES (FUT1 AND SECI) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLITRANSFERASE.
SIMILARITY: BELONGS IO THE GLYCOSYLITRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
6alactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (Secretor blood group alpha-2-fucosyltransferase) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
(Fucosyltransferase 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 GELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 TAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPBILKEFTLHDHVREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 AQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 VFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLIQCNHTIMTIGTFGIWAAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

4093E853E837303B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.1%; Score 1363.5; DB 1; Length 368; 75.9%; Pred. No. 7.5e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADL 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01531; Glyco_transf_11; 1.
                                                                                                                                                                                                                                                                                                                                                         EMBL; Y09882; CAA71008.1; --
EMBL; AF113532; AAD25351.1; --
MGD; MGI:109374; Fut2.
InterFro; IPR002516; GT_11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41464 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal-anchor; Golgi stack DOMAIN 1 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42
195
189
289
315
368 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258;
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Q10983;
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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SOUND THE PETER SOUND TO SOUND THE PETER SOUND TO SOUND THE PETER SOUND TO SOUND THE PETER SOU
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                                                                                                                                                                                                           Hitoshi S., Kushnoki S., Kanazawa I., Tsuji S.;

Molecular cloning and expression of two types of rabbit beta-
molecular cloning and expression of two types of rabbit beta-
galactoside alpha 1.2-fucosyltransferase.";

J. Biol. Chem. 270:8844-8850(1995).

-!- FUNCTION: CREATES A SOLUBLE PRECURSOR OLIGOSACCHARIDE FUC-ALPHA
((1,2)GALBETA-) CALLED THE HANTIGEN WHICH IS AND ESSENTIAL
SUBSTRATE FOR THE FINAL STEP IN THE SOLUBLE AND B ANTIGEN
SUBSTRATES BUT EXHIBIT DIFFERENT KW VALUES.

-!- CAPALITIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP -
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PWQNYHLNDWMSERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 MFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 HFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTIQMSSGNTESPEMRRDSEQHGNGELRG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 YFLFTIFVVSTVFHCHQRLAL------VPAPWAYSARVVVVP-----GHLPREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGD
                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LUMENAL, CÁTALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL).
1E2B831F9DA6CCB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.9%; Score 1319.5; DB 1; Length 354; 73.2%; Pred. No. 3.7e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47; Indels
                    Eukaryota; Metazoa; Chòrdata; Craniata; Vertebrata; Eu:
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Mismatches
                                                                                                                                                                                       MEDLINE=95238380; PubMed=7721792;
Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40035 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X80225; CAA56512.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal-anchor; Golgi stack
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44
197
291
317
354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 248; Conserv
                                                                                                                                 SEQUENCE FROM N.A
                                                                             NCBI_TaxID=9986;
                                                                                                                                                             TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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δλ q

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EMBL; AB005637; BAA31130.1; -. EMBL; AB006137; BAA21741.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BDIX;
                                                                                                                                                                                                                                                                                                           FUT1_RAT O10980;
                                                                 141
                                                                                                                  201
                                                                                                                                          209
                                                                                                                                                                                           269
                                                                                                                                                                                                                                                                                             FUT1_RAT
                                                                                         g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n
                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
1. 21F1D24CFE204106 CRC64;
252 SNGMAWCRENIDASRGDVVFAGNGLEGSPAKDFALLFYQCNHTVMTIGTFGFWAAYLFGGD 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 LTLSVLCSDYHLLK-SPVAMVCLPHPLQTSNGSPSCPEQ-----SSSLSGTWTITPG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 VISTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSI
                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:109375; Fut1.
InterPro; IPR002516; GT_11.
Pfam: PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                         314 TIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1107; DB 1; NA 3.5e-86;
                                      376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Mismatches
                                                                                                                                                                                                                                                                                                                 MEDLINE=97454449; PubMed=9355741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
27
376
328
328
42255 MW; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U90553; AAC53492.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Golgi stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 210; Conservative
                                                                                                               STANDARD;
                                                                                                                                                                                                    (Fucosyltransferase 1).
                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
67
302
328
376 AA;
                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
STRAIN=NIH Swiss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal-anchor;
DOMAIN
                                                                                                              FUT1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                  FUT1_MOUSE
                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
15-UL-1999 (Rel. 38, Last sequence update)
15-UL-1999 (Rel. 41, Last aenotation update)
6alactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
GRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHL 140
                              260 CRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLAN 319
                                                                                                                                                                                                                                                                                                                                                                                   CENIDTSHGDVVFAGNGQEGFPGKDFALLTQCNHTIMTIGTFGFWAAYLAGGDIVYLAN 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDWMEERYRHIPGHFVRFTGYPCSWTFYHLRPEILKEFTLHDHVREEAQAFLRGLRVNG
                                                                                                                                                     SQPS-IFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.
-:- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soejima M., Wang B., Koda Y., Kimura H.: "Two distinct rat GDP-L-fucose:b-D-galactoside 2-alpha-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 FTLPDSEFLKIFRPBAAFLPEWVGINADLSPLQAQFDPWKPDSLFRL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 YTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fucosyltransferase genes.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94280382; PubMed=8010942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 169-310 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fucosyltransferase 1). FUT1 OR FTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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us-10-040-863-8.rsp

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FUT1_HUMAN

ID FUT1_H

EUT1_H

DT 01-FEB

DT 01-FEB

DT 01-FEB

DF 01-FEB

OF 01-FEB

OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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                                                                                                                                                                                                                                                                                                                                         ä;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-ocT-1996 (Rel. 34, Created)
01-oCT-1996 (Rel. 34, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRLGNOMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 NDWMBERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVN- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327
                                                                                                   CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                 21 VISTIIHLOQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: BRAIN.
-!- MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
                                                                                                                                                                                                                                                                                                                                                                                                                38 LTFSVLCPDYHLLK-SPVAMVCLPYPSNASSGSPSCPE------QSLLSGTWTITPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GSQPSTFVGVHVRRGDYVHVMFNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                = GDP
                                                                                                                                                                 LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S.,
"Molecular cloning and expression of two types of rabbit beta-
galactoside alpha 1,2-fucosyltransferase.",
J. Biol. Chem. 270:8844-8850(1995)
-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = G
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
             Interpro; IPR002516; Gr_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgl stack.
                                                                                                                                                                                                                                                                                             54.2%; Score 1102; DB 1; Length 376; 60.1%; Pred. No. 9.6e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                     C350C737C758B7F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 AA
                                                                                                                                                                                                                                                                                                                 Pred. No. 9.66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
MEDLINE=95238380; PubMed=7721792;
                                                                                                                                                                                                                                                     MM.
                                                                                                                                                                 30 376
64 64
302 302
328 328
376 AA; 42416 M
  EMBL; L26009; AAB41514.1;
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Fucosyltransferase 1).
                                                                                                                                                                                                                                                                                                                 Local Similarity
es 209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUT1 OR RFT-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUT1_RABIT
Q10979;
                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                           TRANSMEM
                                                                                                   DOMAIN
                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
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FUT1_RABIT
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01-FEB-1992 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
63-Jactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:Deta-D-galactoside 2-L-fucosyltransferase 1)
Cyalactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
(Fucosyltransferase 1) (Blood group H alpha 2-fugosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASM 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHH 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 VREQIRREFILHDHLREEAQRLLGKLRIGRTGARPRIFVGVHVRRGDYLQVMPQRWKGVV
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                      OF.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUMENAL, CÁTALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
0447A1786231525C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
                         TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS
                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 373;
                                                MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1086.5; DB : Pred. No. 1.9e-84;
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57.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal-anchor; Golgi stack.
DOMAIN 1 12
TRANSMEM 13 29
                                                                                                                                                                                                                                                                                                                                                 EMBL; X80226; CAA56513.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 209; Conservative
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66
301
327
373 AA;
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P19526;
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
Y -> C (IN BOMBAY H-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
-!- POLYMORPHISM: NONFUNCTIONAL MUTANT OF FUT1 ARE THE CAUSE OF THE H-BOMBAY BLOOD GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97445117; PubMed-9299444;

Koda Y., Soejima M., Johnson P. H., Smart E., Kimura H.;

Missense mutation of Full and deletion of Furz are responsible for Indian Bombay phenotype at ABO blood group system.*;

Blochem. Biophys. Res. Commun. 238:21-25(1997).

-!- FOUCTION: CREATERS A SOLUBLE PRECOURSON CLIGOSACCHARIDE FUC-ALPHA (1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN ESSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE SOLUBLE AND B ANTIGEN SYNTHESIS PATHMAY. H AND SE ENTYMES FUCOSYLATE THE SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.

-!- CATALITIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + antimax. Allosyl-1,2-beta-D-galactosyl-R.
                                                                                                                                                       Larsen R.D., Ernst L.K., Nair R.P., Lowe J.B.;
"Molecular cloning, sequence, and expression of a human GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase cDNA that can form the H blood group antigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERMAL OR ENDODERMAL OR GIVEN RESPECTIVELY.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lowe J.B.;
"Molecular basis for H blood group deficiency in Bombay (Oh) and para-Bombay individuals.";
Proc. Natl. Acad. Sci. U.S.A. 91:5843-5847(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94286534; PubMed=7912436;
Kelly_R.J., Ernst L.K., Larsen R.D., Bryant J.G., Robinson J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Polymorphism of the h allele and the population frequency sporadic nonfunctional alleles."; Transfusion 37:284-290(1997).
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 87:6674~6678(1990)
                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A., AND VARIANT ALLELES.
MEDLINE-97240210; PubMed-9122901;
                                                                                                                            MEDLINE=90370848; PubMed=2118655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M35531; AAA52639.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Wagner F.F., Flegel W.A.;
                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT HIS-164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [4]
VARIANT ARG-242
                              NCBI_TaxID=9606
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Q2943 : 0.1910 ;
Cleated)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN - 2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                                                                                                                                                                                                                                                                          183 REFILHDHLREEAQSVLGQLRLGRTGDRPRTFVGVHVRRGDYLQVMPQRWKGVVGDSAYL 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 TIMTIGTFGIWAAXLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA 354
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                            26
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                                                                                                                                                                                                                                                                            12 LAHFLIFVFVTSTIIHLQQ------RIVKLQPLSEKELPMTIQMSSGNTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 KEFTLHDHVREEAQAFLRGLRV--NGSOPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                   DB 1; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96217559; PubMed=8613146;
Cohney S., Mouhtouris E., McKenzie I.F., Sandrin M.S.;
"Molecular cloning of the gene coding for pig alphal-->2
                                                                                                                                                                                                                                               Indels
                                                                   L -> R (IN BOMBAY H-).
/FIId=VAR_009709.
V -> E (IN BOMBAY H-).
/FIId=VAR_019419.
A -> V (IN BOMBAY H-).
/FIId=VAR_019420.
/FIId=VAR_019420.
/FIId=VAR_019421.
W -> C (IN BOMBAY H-).
/FIIId=VAR_019421.
/FTId=VAR_003417.

L -> H (IN PARA-BOMBAY).

/FTId=VAR_009708.

W -> C (IN BOMBAY H-).

/FTId=VAR_003418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND VARIANTS THR-103 AND GLN-286
                                                                                                                                                                                                                                               87;
                                                                                                                                                                                                                   52.0%; Score 1057.5; DB 56.5%; Pred. No. 5.4e-82
                                                                                                                                                                                                                                               46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenetics 44:76-79(1996).
                                                                                                                                                                                        41251 MW;
                                                                                                                                                                                                                                               Matches 205; Conservative
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                                                                       242
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                164
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                                                                                                                                                                                      365 AA;
                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                164
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                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                   Best Local
                VARIANT
                                           VARIANT
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MEDLINE=97468270; PubMed=9321466;

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LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 PMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 PVAIFCLAGTPVHPNASDSCPKH-PASLSGTWTIYPDGRFGNQMGQYATLLALAQLNGRQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 AFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMP 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 341
                                                                                                                                                       Meijerink E., Necessity, Meijerink E., Necessity E., Dinter A., Bertschinger H.O., Stranzinger G., Voegeli P.:

"Expression and activity of porcine alpha(1,2) fucosyltransferases determine erythrocyte antigen precursor O status and susceptibility tescherichia coli F18 colonization in the small intestine.";

Submitted (Mar.1999) to the Embi-Genank/DBH databases.

-: CATALYNIC ACTIVITY: GPD-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1.2-beta-D-galactosyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Meijerink E., Fries R., Voegeli P., Masabanda J., Wigger G., Stricker C., Neuenschwander S., Bertschinger H.U., Stranzinger G.; "Two alpha(1,2) fucosyltransferase genes on porcine chromosome 6q11 are closely linked to the blood group inhibitor (S) and Escherichia coli F18 receptor (ECTIRR) loci."; Mamm. Genome 8:736-741(1997).
                                                                                                                                                                                                                                                                                                 -!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CIGTERNAE OF GOLGI.
-!- MISCELLANBOUS: THERE ARE IWO GENES (FUTI AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER.
-!- SIMILARITY: BELONGS IO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF136896; AAF59833.1; -.
Interpro: IPR002516; GT_11.
Pfan: PF01531; GYO-C transf_11; 1.
Transferase: Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.7%; Score 1050.5; DB 1; Length 365; 62.9%; Pred. No. 2.1e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> F (IN REF. 1).
DAFCE77E89A29D75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Golgi stack; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41106 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L50534; AAB02984.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB81884.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 62.9
Matches 195; Conservative
                                                                                                                                        TISSUE-Small intestine;
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355
301
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103
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65
301
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77
365 AA;
                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U70883;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL cutstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUC-ALPHA (1.2) GALBETA-) CALLED THE HANTGEN WHICH IS AN BSSENITAL SUBSTRATE FOR THE FINAL STEP IN THE MEMBRANE-ASSOCIATED A AND B ANDIGEN SYMPHESIS PATHWAY. HAND SE BNITHES FUGGELATE

-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1.2. beta-D-galactosyl-R.
-!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE IN MEMBRANE PROTEIN. MEMBRANE-BOUND GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER.
290 PARDFALLVQCNHTIMTIGTFGFWAAYLAGGDTIYLANFTLPTSSFLKIFKPEAAFLPEW 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OLIGOSACCHARIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 PAKDFALLIQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 341
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAMCRENINASRGDGVFAGNGIEGS 60
                                                                                                                                                                                                                                                                              (Secretor blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piau J.-P., Labarriere N., Dabouis G., Denis M.G.; "Evidence for two distinct alpha(1,2)-fucosyltransferase genes differentially expressed throughout the rat colon."; Biochem. J. 300:623-626(1994).
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Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
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                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
3alactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (Secrett group alpha-2-fucosyltransferase) (GDF-L-fucose.beta-0-galactoside 2-alpha-L-fucosyltransferase 2) (Ripha(1,2)FT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14DECEB7C2E6384A CRC64;
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                                                                                                                                                                          159 AA
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                                                                                                                                                                          PRT;
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                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                      FUT2 OR SEC1 OR FIB.
                                 342 VGIPADLSPL 351
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                                                              350 VGINADLSPL
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98
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                                                                                                                                                                                                               01-OCT-1996
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                                                                                                                                                                          FUT2_RAT
Q10984;
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TRANSMEM
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VGLD_HSVEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
   61 PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 HNKATKVPLSEKCCIFDNPDKFNNISSEYLHLTGHFYQ-----SWKYF----- 172
                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Created)
15-570N-2002 (Rel. 41, Last sequence update)
15-570N-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase C06E1.7 in chromosome III (EC 2.-.-.).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 STARLANHIFELVSVYGMAKSLNRKPAIFVEDSKYNLLITGVRKVLPGLLDEFQIFEYPV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 --TAKKIP-----MQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 TLHDHVREEAQAFLRGL----RVNGSQPSTFVG---VHVRRGDYV---HVMPNVWKGVVA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          '2.2 Mb of contiguous nucleotide sequence from chromosome III of
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 1; Length 365; 7.9e-07;
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48; Mismatches 115; Indels
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Hypothetical protein; Transferase; Glycosyltransferase.
SEQUENCE 365 AA; 41991 MW; B5FBCA363F31977F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 VGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                  YKQ7_CAEEL
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                                                                                                                                                                                                                    RESULT 12
YKQ7_CAEEL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91082407; PubMed=1845821; Flowers C.C., Eastman E.M., O'Callaghan D.J.; "Sequence analysis of a glycoprotein D gene homolog within the unique short segment of the EHV-1 genome.";
---DKYKEKVQSFVKPAIDFSPLPNSDSSNFISRICIHIRRTDFVDGOHHSSNV----- 223
                                                                   -- YSSPVFVVTSNGMAWCRENINASRGD 270
                                                                                                                                                                                                                                278 KYFVS---ENIPQDDLAYSHYSCDATLITAPSSTFGWWLGYLSKGQAVYYQDIRSINDVN 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92263756; PubMed=1316673; Colla C.F. III, Flowers C.C., O'Callaghan D.J.; Colle C.F. III, Flowers C.C., O'Callaghan D.J.; Colle C.F. III, Flowers C.C., O'Callaghan D.J.; Collaboration of protein kinase, homolog of glycoprotein gx of pseudorabies virus, and a novel glycoprotein map within the unique short segment of equine herpesvirus type 1."; Virology 188:545-557(1992).
                                                                                                                        --SFIKPALEFIKEREQKDVNKKMLTVIMGDDPDFEAKMF----EGTVRAKKEAKIEETT
                                                                                                                                                                                        271 VVFAGNGIEGSPAKDFALL-TQCNHTIMTI--GTFGIWAAYLAGGDTIYLANY-TLPDSP
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N-LINKED (GLCNAC. .) (POIENTIAL).
N-LINKED (GLCNAC. .) (POIENTIAL).
N-LINKED (GLCNAC. .) (POIENTIAL).
323CDCA9C9762F05 CMC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Equine herpesvirus type 1 (strain Kentucky A) (EHV-1). Viruses; dSDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus. NCBL_TaxID=10329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein D precursor (Glycoprotein 17/18) GD OR GP17/18 OR 72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442, AA.
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Pred. No. 3.2;
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Pfam; PF01537; Herpes_glycop_D; 1.
Glycoprotein; Signal; Transmembrane.
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EMBL; M87497; AAA46073.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                       327 FLK-VFKPEAAFLPEWVGIPAD 347
                                                                                                                                                                                                                                                                                                                                                                                    335 YKKGVLDPDDFFVPSWTSIMLD 356
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396
442 AA;
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     Query Match
Best Local
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                                                                                                                                                                                   136 QNYHLNDWMEERYRH----IPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQ 190
                                                                                                            78 NSIGRLGNQMGEYAT -- LFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPW 135
                                                                                                                                                    ----FARPVPP 331
                                                                                                                                                                                                                        DNHPGFDSVESEITQNKTDPKPGQADPKPNQPFKWPSIKHLVPRL------DEVDEVIE 384
                                                                       234 LYRRVIEIDGRRIXTDFSVTIPSERCPIAFELNFGN---PDRCKTPEOYSRGE---VFTR 287
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujiwara T., Morishima S., Takkhashi I., Hamada S.,
"Molecular cloning and sequencing of the fimbrilin gene of
Porphyromonas gingivalis strains and characterization of recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION. Finbrillin is the structural subunit of the fimbriae, that are filamentous appendages on the cell surface. Funbriae of P. gingivalis are recognized as a major virulence factor as they mediate cell adhesion and play an important role in invasion of
                                    LQQRIVKLQ------PLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTI 77
                                                                                                                                                                                                                                                          191 AFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gingivalis and their effects on adhesion to and invasion of human epithelial cells.";
Infect. Immun. 70:277-285(2002).
                                                                                                                                                                                                                                                                                    385 PVIKPPKTSKSN-STFVGISVGLGIAGLVLVGVGLLYVCLRR---KKELKVCTERLDSP
                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Major fimbrial subunit protein, type III precursor (Fimbrillin)
   50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    periodontal tissues.
SUBCELLULAR LOCATION: Fimbria.
SIMILARITY: BELONGS TO THE P.GINGIVALIS FIMBRILLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Functional differences among FimA variants of Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakagawa I., Amano A., Kuboniwa M., Nakamura T., Kawabata S.
Hamada S.;
 31; Mismatches 103; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides; Bacteroidales;
                                                                                                                                              288 RFLGEFNFPQGEHMTWVKFWFVYDGGNL---PVOFYEAQA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 197:241-247(1993).
                                                                                                                                                                                                                                                                                                                                                                                          353 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION, AND CLASSIFICATION INTO TYPES.
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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NCBI_TaxID=837;
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MEDLINE=94071950; PubMed=7902712;
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38024 MW;
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54; Conservative
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353 AA;
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051826;
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MEDLINE=20139694; PubMed=10673428;
Hallberg B.M., Bergfors T., Boeckbro K., Pettersson G., Henriksson G.,
                                                                                                                                                                                                                                                                                                                                                         80 LTIELTEGNQEAAGLIMTAEPVEVTLVAGN-----NYYGYDGSQGGNQISQGTPLE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----IPWQNYHLNDWMBERYRHI-----PGHFVRFTGYPCSWTFYHH--LRPEIL- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 TTFNGAYSPANYTHVDWLGRDYTEIGAATVNTFKGF----YVLESTYAQNAGLRFTILC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --KEFTLHDHV----REEAQAFLRGLRVNGSQPSTF--VGVHVRRGDYVHVMPNVWKGVV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 VKGKLTKHDGTALSSEEMTAAFNAGWIVANNDFTTYYPVLVNFESNNYTYTGEAVEKGKI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoded
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                                                                                          Gaps
                                                                                                                                                             45 MTTQMSSGNTESPEMRRDSEQ-----HGNGELRGMFTINSIGRLGNQMG---EYAILFA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Basidiomycota; Hymenomycetes; Homobasidiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDH_PHACH STANDARD; PRT; 773 AA.

Q01738: 000047;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cellobiose dehydrogenase precursor (EC 1.1.5.1) (CDH) (Cellobiose-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quinone = cellobiono-1,5-
                                                                                      78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97176414; PubMed=9023960;
Li B., Nagalla S.R., Renganathan V.;
"Cellobiose dehydrogenase from Phanerochaete chrysosporium is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A new scaffold for binding haem in the cytochrome domain of extracellular flavocytochrome cellobiose dehydrogenase."; Structure 8:79-88(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 ADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGI 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 VRNHKFDINLTITGPGINNPENPIT------ESANLNVNCVVAAWKGV 347
Score 89; DB 1; Length 353; Pred. No. 3.6;
                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ø
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"Cloning of a cDNA encoding cellobiose dehydrogenase, hemoflavoenzyme from Phanezochaete chrysosporium.";
Appl. Erviron. Microbiol. 62:1329-1335(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Secreted. SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO
                                                                              Mismatches 110;
                                                                                                                                                                                                                                                                                                          96 LARMNGRLAF -- IPASMHNALAPIFRISLPVLHSDTAKK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Fungi, Basidiomycota, Hymenomycete
Aphyllophorales, Corticiaceae, Phanerochaete.
NCBI_TaxID=5306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appl. Environ. Microbiol. 63:796-799(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Cellobiose + a lactone + a phenol.
-!- COFACTOR: ONE FAD AND ONE HEME B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97077226; PubMed=8919793;
                                                                                  38;
                                       22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phanerochaete chrysosporium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OXIDOREDUCTASES FAMILY.
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO CELLOBIONOLACTONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quinone oxidoreductase).
CDH-1 AND CDH-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        two allelic variants.
                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-OGC10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HID DEBTAL BARKER BARKE
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                          Ouery Match 4.4%; Score 89; DB 1; Length 773; Best Local Similarity 22.0%; Pred. No. 9.3; Matches 49; Conservative 29; Mismatches 91; Indels
                                                                                                                                                                                                                                                                            FAD (ADP PART) (PCTENTIAL).
54F721E779AA4D7B CRC64;
                                                                                                                                                                                                                             CELLOBIOSE DEHYDROGENASE
                                                                                                                                                                                                                                     HEME DOMAIN.
OXIDOREDUCTASE.
HEME LIGAND.
HEME LIGAND.
                                                                                                                                                                                                                                                        83 HEN
181 HEN
265 FAI
82007 MW;
                                                                                                                                                                                                                           19
19
235
83
181
236
773 AA;
                                                                                                                                                                                                                                                                 BINDING
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                    DOMAIN
DOMAIN
BINDING
                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                            CHAIN
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205 TFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENI 264 | : | | : | | | | | | 397 T------INDNPNYKDHVF---GY--SAFDFLNGKRAGPVATYLQTALA--RPNF 438 265 ----NASRGDVVFAGNGIEGSPAKD------FALLTQCNHTIMTIGTFG----IWAAYL 309 439 TEKTNYMYSNYVRNGSQILGVQTNDPTLGPNGFIPVTPKGRVILSAGAFGISRILFQSGI 498 153 GHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRG------LRVNGSQPS 204 310 AGGDTIYLANYTLPDSPFLKVFKPEAAFLP---EWVGIPADLS 349 Q QΫ gg qq Qy δλ

11;

Gaps

54;

Search completed: May 27, 2003, 15:07:12 Job time : 22.122 secs

```
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

May 27, 2003, 14:52:27 ; Search time 45.4049 Seconds

Run on:

(without alignments) 1050.630 Million cell updates/sec

Perfect score:

US-10-040-863-8\_COPY\_23\_380 1921 1 STIIHLQORIVKLQPLSEKE......RSHFHLKAKGVICXVAGRAF

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

908470 Total number of hits satisfying chosen parameters: 908470 segs, 133250620 residues

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Natch 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_101002:\* •• Database

| SIDS2/goddata/geneseqgpenesqp-embl,AAl198b, DAI:\*
| SIDS2/goddata/geneseqgpenesqp-embl,AAl198b, DAI:\*
| SIDS2/goddata/geneseqg-embl,AAl199b, DAI:\*
| SIDS2/goddata/geneseqgeneseqg-embl,AAl199b, DAI:\*
| SIDS2/goddata/geneseqgenes /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*/SIDS2/gcgdata/geneseqp-embl/AA1984.DAT:\*/SIDS2/gcgdata/geneseqp-embl/AA1985.DAT:\*/SIDS2/gcgdata/geneseqp-embl/AA1985.DAT:\*/SIDS2/gcgdata/geneseqp-embl/AA1986.DAT:\*/SIDS2/gcgdata/geneseqfyeneseqp-embl/AA1987.DAT:\*/SIDS2/gcgdata/geneseqfyeneseqp-embl/AA1987.DAT:\*/SIDS2/gcgdata/geneseqfyeneseqp-embl/AA1987.DAT:\*/SIDS2/gcgdata/geneseqfyeneseqp-embl/AA1988.DAT:\*/SIDS2/gcgdata/geneseqfyeneseqp-embl/AA1988.DAT:\* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\* /SIDS2/gcgdata/geneseg/genesegp-embl/AA1982.DAT:\* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA198 10: 18: 20: 20: 22: 23:

chance to have a result being printed, Pred. No. is the number of results predicted by chance to score greater than or equal to the score of the result being and is derived by analysis of the total score distribution

## SUMMARIES

|   | Description                 | Rat heratoma man o | Rat henatoms man | Dat honotons use o | Rat honatoma 1135 c | Doroing acceptor t | ביום בסידסידטברסו ב | Himse Good protein | Himan Secs processing | GDD-Fug.bots-D-21 | GDP-I-fucese-beta- |
|---|-----------------------------|--------------------|------------------|--------------------|---------------------|--------------------|---------------------|--------------------|-----------------------|-------------------|--------------------|
|   | ID                          | AAB36104           | AAE16622         | AAB36105           | AAE16623            | AAW37855           | AAW53101            | AAW69332           | AAB36106              | AAR13751          | AAR80154           |
|   | DB                          | 21                 | 23               | 21                 | 23                  | 19                 | 6                   | 19                 | 2                     | 12                | 16                 |
|   | Query<br>Match Length DB ID | 380                | 380              | 353                | 353                 | 340                | 340                 | 343                | 344                   | 365               | 365                |
| * | Query<br>Match              | 100.0              | 100.0            | 98.7               | 98.7                | 75.5               | 75.5                | 73.3               | 72.7                  | 54.7              | 54.7               |
|   | Score                       | 1921               | 1921             | 1896               | 1896                | 1451               | 1451                | 1407.5             | 1397                  | 1051.5            | 1051.5             |
|   | Result<br>No.               | П                  | 2                | e                  | 7                   | ι'n                | 9                   | 7                  | œ                     | 6                 | 10                 |

| 2-Alpha-fucosvitra | Alpha-fucosyl | uman H-transfera | alnha 1 2 fi | alpha(1,2 | an H-transf | id H transferase | ig albha-1-2 f | 9        | wine alpha(1.2 | wine alpha-1,2 | glycosyltrans | sevis alpha- | n secreted | H. pylori UA802 al | licobacter | acteroides | ropionibac | Human protein cont | h Fao    | aan      | ovel     | humi     | polypeptid | Amino acid sequenc | Propionibacterium | nas       | Human protein sequ | l Signal t | qenesis a | a nemnu  | l human secr | mic      | human diac | n GRB-2. Ho |
|--------------------|---------------|------------------|--------------|-----------|-------------|------------------|----------------|----------|----------------|----------------|---------------|--------------|------------|--------------------|------------|------------|------------|--------------------|----------|----------|----------|----------|------------|--------------------|-------------------|-----------|--------------------|------------|-----------|----------|--------------|----------|------------|-------------|
| AAR70422           | 40            | AAR90572         | AAW23805     | AAW13640  | AAY97279    | AAW53102         | AAY79302       | AAB47995 | AAW97356       | AAW30630       | AAR45936      | AAY17969     | AAG03530   | AAY92713           | AAG64071   | AAM51992   | AAU39722   | AAE20142           | AAR26061 | AAY70408 | ABG10624 | ABG28599 | AAM93762   | AAY54126           | AAU46700          | AAR61993. | AAB93020           | AAU17082   | AAE11890  | ABB97219 | AAU30862     | ABB57107 | ABG25048   | AAR85918    |
| 16                 | 16            | 17               | 18           | 18        | 21,         | 61               | 21             | 23       | 20             | 20             | 15            | 20           | 21         | 21                 | 22         | 23         | 22         | 23                 | 13       | 21       | 22       | 22       | 22         | 21                 | 22                | 16        | 22                 | 22         | 22        | 23       | 22           | 23       | 22         | 16          |
| 365                | 365           | 365              | 365          | 365       | 365         | 365              | 355            | 365      | 365            | 365            | 365           | 357          | 110        | 300                | 300        | 287        | 661        | 069                | 317      | 355      | 1515     | 1073     | 984        | 586                | 604               | 353       | 394                | 1031       | 2057      | 2058     | 1416         | 217      | 629        | 217         |
| 4                  | 4.            | 4                | 4.           | 4.        | 4           | 4.               | 4.             | √"       | ₹.             | 54.4           | 4.            | H.           | 'n,        |                    | •          | •          |            |                    |          |          |          | •        | •          |                    |                   |           |                    |            |           | 4.6      | •            |          | 4.6        | 4.5         |
| 05.                | 05.           | 05               | 05.          | 05        | 05.         | 046              | 046            | 046      | 044            | 1044.5         | 04            | O١           | 288.5      | 141                | _          | 139.5      | 103        | 101                |          | 96.5     | 9<br>D   | 93       |            | 89.5               | O١                | 88        | 88                 | 86         | 88        |          | 88.5         | 88       | 88         | 87          |
| 11                 | 12            | 13               | 14           | 15        | 16          | 17               | 18             | 19       | 20             | 21             | 22            | 23           | 24         | 25                 | 26         | 27         | 28         | 29                 | 30       | 31       | 32       | 33       | 34         | 32                 | 36                | 37        | 38                 | 90         | 40        | 41       | 42           | 43       | 44         | 45          |

## ALIGNMENTS

RESULT 1

Rat hepatoma H35 cell alphal-2fucosyltransferase. AAB36104 standard; Protein; 380 AA (first entry) small cell lung carcinoma 19-FEB-2001 AAB36104; AAB36104 

Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Calbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease;

Rattus norvegicus.

WO200064464-A1.

23-APR-1999; 02-NOV-2000.

99WO-US07384.

99WO-US07384 23-APR-1999; (PACI-) PACIFIC NORTHWEST CANCER FOUND, Holmes EH, Sherwood AL;

WPI; 2000-687262/67.

N-PSDB; AAC67965

New rat ganglioside GM1-specific alpha1-2Fucosyltransferase, useful for

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301
                 THE HERE RAY NOW A PROPERTY OF THE PROPERTY OF
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                                                                                                                                 The present sequence was given in a specification relating to an isolated rat ganglioside GM_1-specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising frucalphal-2Galbetal-3GalNac, a glycolipid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoprotein, glycolipoprotein or oligosaccharide having a terminal glycoprotein, glycolipoprotein or oligosaccharide having a terminal compacting the protein with GDP-fucose and ganglioside GM_1 The contacting the protein with GDP-fucose and ganglioside GM_1. The contacting the protein with GDP-fucose and ganglioside GM_1 The contacting the protein with GDP-fucose and ganglioside GM_1 cobtained glycoproteins, glycolipoproteins, glyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
     useful as a nutritional composition neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STIIHLQQRIVKLQPLSEKELPMTTQMSSGNIESPEMRRDSEQHGNGELRGMFTINSIGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat; alphal-2fucosyltransferase; alphal-2FucT; antisense therapy; galactose betal-3N-acetylgalactosamine; Galbetal-3GalNAc; glycolipid; glycoprotein; glycolipoprotein; oligosaccharide; fucosyl-GM1; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1921; DB 21; Length 380;
Pred. No. 2.7e-201;
0; Mismatches 0; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..27
/note= "Intracellular/Transmembrane domain"
199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
preparation of fucosyl GM1 which is or immunotherapeutic for cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H35 cell alphal-2FucT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE16622 standard; Protein; 380 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; ; 100.0%; 1
                                                                               Claim 1; Fig 5; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 358; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell transformation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE16622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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AAE16622
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(allphal-ZFucT) enzyme and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate moiety found in ganglioside GML, at terminal galactose betal-3N-acety/galactosamine (Galbetal-3GalNAc) accharide. Alphal-ZFucT DNA is useful for producing rat alphal-ZBucT DNA is useful for producing rat alphal-ZFucT DNA is useful for detecting oncognic transformation which alphal-ZFucT DNA is useful for detecting oncognic transformation which alphal-ZFucT is activated in cell transformation, antisense sequences derived from alphal-ZFucT DNA are useful for inhibiting, suppressing or treating cancer. Alphal-ZFucT DNA is useful in gene therapy and all the present sequence is rat hepatoma H35 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat hepatoma H35 celi alphal-2fucosyltransferase, useful for producing GMJ-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to rat GM1-specific alphal-2fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 STIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCXVAGRAF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
/note= "N-glycosylated"
221..380
/note= "Region which overlaps rat FTB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1921; DB 23;
illarity 100.0%; Pred. No. 2.7e-201;
Conservative 0; Mismatches 0;
                                                                                                           /note= "N-glycosylated"
                                                                                                                                                                  /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Fig 5; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              99us-0298886
                                                                                                                                                                                                                                                                                                                                       99US-0298886
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NWHO-) NORTHWEST HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-121132/16.
N-PSDB; AAD27207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 358; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 AA;
                                                                              Modified-site
                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                       23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                        23-APR-1999;
                                                                                                                                                                                                                         US6329170-B1
                                                                                                                                                                                                                                                                             11-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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323 PDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 380

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186 GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
172
                                                                                                                                                                                                                                                      AAE16623 standard; Protein; 353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Fig 3; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0298886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NWHO-) NORTHWEST HOSPITAL.
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holmes EH, Sherwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-121132/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-121132,
N-PSDB; AAD27208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                           Rat hepatoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1999;
                                                                                                                                                                                                                                                                                                                          09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                     301
                                                                 246
                                                                                                                                                                                                                                      AAE16623
                                                                                                                                                                                                                                                                        δ
                            Dp
                                                                 \delta
                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is given in a specification relating to a rat ganglioside GM 1-specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising rucalphal-2Galbetal-3GalNac, a glycolipid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising Fucalphal-2Galbetal-3GalNac. The method involves contacting alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoprotein, glycolipoprotein or oligosaccharide having a terminal Galbetal-3GalNac group. It is also useful for synthesis of fucosyl-GM_1 by contacting the protein with GDP-fucose and ganglioside GM_1. The obtained glycoproteins, glycolipids and oligosaccharides are useful as nutritional compositions and fucosyl-GM_1 is useful for inducing an intrinsipal compositions and fucosyl-GM_1 is useful for inducing an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVRBEAQAFLRGLRVNGSQPSTFV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                             Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Calberal-3GalNAc; immunotherapy; immunosupprassion; cancer; neurological disease; sanali cell lung carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LQORIVKLQPLSEKELPMTIQMSSGNTESPEMRRDSEQHGNGELRGMFIINSIGRLGNOM 60
                                                                                                                                                            Rat hepatoma H35 cell alphal-2fucosyltransferase catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.7%; Score 1896; DB 21; 100.0%; Pred. No. 1.3e-198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PACI-) PACIFIC NORTHWEST CANCER FOUND.
                                                          AAB36105 standard; Protein; 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 3A; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US07384
                                                                                                                                                                                                                                                                                                                                                                                      99WO-US07384
                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 353; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sherwood AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-687262/67.
N-PSDB; AAC67966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 AA;
                                                                                                                                                                                                                                                                                   Rattus norvegicus
                                                                                                                                                                                                                                                                                                                   WO200064464-A1.
                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-1999;
                                                                                                                            19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holmes EH,
                                                                                            AAB36105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                            RESULT 3
                                        AAB36105
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(alphal-2Fucr) enzyme and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate moiety found in ganglioside GM1, a terminal galactose betal-3N-acetylgalactosamine (Galbetal-3GalNac) saccharide. Alphal-2Fucr DNA is useful for producing rat alphal-2Fucr protein by recombinant techniques. Alphal-2Fucr DNA is useful for proper protein by recombinant techniques. Alphal-2Fucr DNA is useful for the preparative synthesis of fucosyl containing glycolipids, glycoproteins, glycolipoproteins and oligosaccharide, and for preparing fucosyl-GMI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for producing GMI-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues
                                                                                                                         305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat; alphal-2fucosyltransferase; alphal-2fucT; antisense therapy; galactose betal-3Nacetylgalactosamine; Galbetal-3GalNoc; glycolipid; glycoprotein; glycolipoprotein; oligosaccharide; fucosyl-GM1; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GM1; cell transformation; catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to rat GMI-specific alphal-2fucosyltransferase
RGDVVFAGNGIEGSPAKDFALLIQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                                                                                                                                               306 LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 358
                                                                                                                                                                                                                                                                                                                    /note= "Region which overlaps rat FTB"
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H35 cell alphal-2FucT catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-glycosylated"
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Alphal-2FucT DNA is useful for detecting oncogenic transformation which
           involves assaying for changes in expression of alphal-2 Fucr. Since alphal-2Fucr is activated in cell transformation, antisense sequences derived from alphal-2Fucr DNA are useful for inhibiting, suppressing or treating cancer. Alphal-2Fucr DNA is useful in gene therapy and antisense therapy. The present sequence is rat hepatoma H35 cell alphal-2Fucr catalytic domain.
                                                                                                                                                                                                                                                                                                           185
                                                                                                                                                                                                                                                                                                                                                                 245
                                                                                                                                                                                                                                                                                                                                                                                                                     305
                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                        GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 125
                                                                                                                                                                                                                                                                            GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                   Gaps
                                                                                                                                                                                            LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 65
                                                                                                                                                                                                          1 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM
                                                                                                                                                                                                                                                                                                                                                                               GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAMCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                    RGDVVFAGNGIEGSPAKDFALLTQCNHTIMIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                    YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
                                                                                                                                                                                                                                                                                                                                                              GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 358
                                                                                                                                      Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secretor; glycosyltransferase; FUT2; pig; epitope; antige
transgenic animal; xenotransplantation; organ transplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..4
/note= "N-terminal cytoplasmic tail"
                                                                                                                                      98.7%; Score 1896; DB 23;
100.0%; Pred. No. 1.3e-198;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Asn is N-glycosylated"
251..253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Asn is N-glycosylated'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Asn is N-glycosylated"
305..307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Asn is N-glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5..26
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "C-terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porcine secretor transferase (FUT2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW37855 standard; Protein; 340 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C
185..187
                                                                                                                                                 Best Local Similarity 100.
Matches 353; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279..281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                           353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09807837-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sus scrofa
                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW37855;
                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jomain
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                                                                                                                                                                                                                                                                                                                                                              186
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2222222X
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                                                                                                                                                                                                                                                                                                                                  ΩQ
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                                                                                                                                                                                                                                                                                                      {}^{Q}_{\lambda}
                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                                                     QQ
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This polypeptide comprises porcine secretor glycosyltransferase (SE or FUT2), a type II integral membrane protein has high affinity for type I and type III substrates. Its amino acid sequence was deduced from the nucleotide sequence of a genomic DNA clone (see AAV29003) isolated from a pig liver library on the basis of homology to human FUT2 cDNA. Pig FUT2 shows 83.2% identity with human FUT2. Expression of a glycosyltransferase, such as porcine Se, in a tissue results in reduced expression of unwanted carbohydrate pancreas, rendering if more suitable for transplantation, i.e. less immunogent and of increased immunological acceptablity. A claimed method of producing a cell from a donor species that is immunologically acceptable to a recipient species involves reducing levels of carbohydrate on the donor cell that causes it to be recognised as non-sell by the recipient by expressing a nucleic acid for a glycosyltransferase such as porcine Se in the cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVN3SQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 STITHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                      Nucleic acid encoding glycosyltransferase able to compete with second such enzyme - particularly used to reduce expression of unwanted carbohydrate epitope(s) on tissues intended for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.5%; Score 1451; DB 19;
81.9%; Pred. No. 6.8e-150;
tive 26; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDSPFIKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
                                                                                                                                                                                                                                                                       Claim 6; Fig 1A-B; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW53101 standard; Protein; 340
               97WO-AU0054C.
                                           96AU-0001823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 81.9% Matches 271; Conservative
                                                                                                            Sandrin MS
                                                                           (AUST-) AUSTIN RES INST
                                                                                                                                        WPI; 1998-169148/15.
N-PSDB; AAV29003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 AA;
                                                                                                                                                                                                                                         transplantation
                                                                                                          McKenzie IFC,
               22-AUG-1997;
                                           23-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW53101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
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(first entry)

08-JUL-1998

NAMES OF COLOR OF STREET STREE

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This sequence is the human Sec2 protein of the invention. The DNA encodes a alpha(1,2) fucosyltransferase and is the Secretor alpha(1,2) fucosyltransferase locus, that cross hybridises with the H blood group alpha(1,2)fucosyltransferase gene. The DNA is useful for producing a recombinant human GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase (FOT2) which can be used for genotyping an individual as a secretor or nonsecretor as it is known that nonsecretors homozygous for a mutant allele of the FOT2 gene that has a stop codon in the position corresponding to amino acid 143.
                                                                                                                                                                                    Sec2; alpha(1,2) fucosyltransferase; H blood group; secretor genotyping; GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSTEVGVHVRRGDYVHVMPNVWRGVVADRGYLEKALDMFRARYSŠPVFVVTSNGMAWCRE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STITHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STIFHVOORLAKIQAM - WELPV - - - - - OIPVLASTSKALGPSOLRGMWTINAIGR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant enzyme and genotyping person as secretor or nonsecretor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding fucosyltransferase enzyme - useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rouguier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.3%; Score 1407.5; DB 79.2%; Pred. No. 4e-145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lennon G, Lowe JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Column 45-50; 55pp; English.
                                     AAW69332 standard; Protein; 343
                                                                                                                                                                                                                      FUT2; nonsecretor genotyping.
                                                                                                                                                Human Sec2 protein sequence
                                                                                                                                                                                                                                                                                                                                                                      95US-0395800
                                                                                                                                                                                                                                                                                                                                                                                                        95US-0395800
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 79.2 Matches 262; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kelly RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                        GIORGI D.
KELLY R J.
LENNON G.
LOWE J B.
ROUQUIER S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-520127/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV58323
                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      28-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-1995;
                                                                                                                                                                                                                                                                                              US5807732-A.
                                                                                                              20-NOV-1998
                                                                                                                                                                                                                                                                                                                                  15-SEP-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Giorgi D,
                                                                         AAW69332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KELL/)
(LENN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LOWE/)
(ROUQ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            (GIOR/)
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 RESULT 7
                 AAW69332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents pig secretor used in an example of the present invention. The present invention describes nucleic acids (NA) encoding a chimeric glycosyltransferase. The NAs comprise a catalytic domain of a first glycosyltransferase (GT) and a localisation signal of a second GT, whereby when the NA is expressed in a cell and where the chimeric enzyme is located in a mera of the cell where it is able to compete for substrate with a second GT, resulting in reduced levels of a product from the second GT. The NAs can be used to produce cells and organs with desired glycosylation patterns. Products and methods of the expitopes in cells, tissues or organs which may be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding chimeric glycosyltransferases - used for altering carbohydrate levels on the surface of cells, useful in gene therapy and transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STITHLOORIVKLOPLSEKELPMTTOMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 340;
                                  Pig; secretor; chimeric; glycosyltransferase; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 75.5%; Score 1451; DB 19; Best Local Similarity 81.9%; Pred. No. 6.8e-150; Matches 271; Conservative 26; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDSPFLKLFKPEAAFLPEWIGIEADLSPLLK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 6; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transplantation or gene therapy
                                                                                                                                                                                                                                   96US-0024279.
                                                                                                                                                                                                 97WO-AU00492
                                                                                                                                                                                                                                                                                                                              Sandrin MS;
                                                                                                                                                                                                                                                                                        (AUST-) AUSTIN RES INST.
                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-159170/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 AA;
                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV21639
                                                     transplantation.
                                                                                                                                                                                                                                                                                                                              McKenzie IFC,
                                                                                                                                                                                                 01-AUG-1997;
                                                                                                                                                                                                                                   21-AUG-1996;
02-AUG-1996;
                                                                                                                         W09805768-A1
                                                                                                                                                             12-FEB-1998
                                                                                       Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
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Pig
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QYg δλ q QΥ g õ q òλ g δy

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Gaps

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AAR13751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lowe JB;
     72
                                                                                             192
                                                                                                                   240
                                                                                                                                          252
                                                                                                                                                               300
                           121
                                                                                                                                                                                                                                  AAR1375
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                                                                                                                                          QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is given in a specification relating to a rat ganglioside GM.1-specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-2Galbetal-3GalNAc, a glycolipid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising Fucalphal-2Galbetal-3GalNAc. The method involves contenting alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoprotein, glycolipoprotein or oligosaccharide having a terminal Galbetal-3GalNAc group. It is also useful for synthesis of fucosyl-GM.1 by contacting the protein with GDP-fucose and ganglioside GM.1 The obtained glycoproteins, glycolipids and oligosaccharides are useful as nutritional compositions and fucosyl-GM.1 is useful for inducing an increase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
                                                                                                                                                                                                              neuroprotective; nootropic; gene therapy; Pucalphal-2Galbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease; small cell lung carcinoma.
NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.7%; Score 1397; DB 21; 78.9%; Pred. No. 5.7e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                         PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                                                                                                                                                                                                                                                                                          (PACI-) PACIFIC NORTHWEST CANCER FOUND.
                                                                                                                         AAB36106 standard; Protein; 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 3B; 91pp; English.
                                                                                                                                                                                           Human Sec2 catalytic domain.
                                                                                                                                                                                                                                                                                                                                            99WO-US07384
                                                                                                                                                                                                                                                                                                                                                                   99WO-US07384
                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 262; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Sherwood AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-687262/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 AA;
                                                                                                                                                                                                                                                                                               WO200064464-A1.
                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   23-APR-1999;
                                                                                                                                                                                                                                                                                                                                            23-APR-1999;
                                                                                                                                                                     19~FEB-2001
                                                                                                                                                                                                                                                                                                                      02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                Holmes EH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local
                     252
                                            301
                                                                                                    RESULT 8
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WMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGS 179
                                                                                                                                                                   QPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCR 239
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The amino acid sequence codes for a protein capable of functioning as a GDP- Fuc:[beta-D-Gal alpha(1,2)- fucosyltransferase. The functional protein is represented by amino acids 33 to 365. The enzyme produced by the DNa sequence can be used in enzymatic fucosylation of chain-terminating galactose residues on lactoseamine or neolacto type beta-D-galactoside to alpha-2-L-fucose residues. See also AAR13749-R13752.
                                                                                                                                                                                               ENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolation of gene conveying post-translational characteristic e.g. the presence of soluble or membrane bound oligo or polysaccharide or glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.7%; Score 1051.5; DB 12; Lengt
63.3%; Pred. No. 4.3e-106;
ive 37; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                  LPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 3; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR13751 standard; Protein; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90US-0479858.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNMI ) UNIV OF MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-267151/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycosyltransferase.
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Matches 195; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR13751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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14-FEB-1990;
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LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120

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23 STIFHVQORLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGMWIINAIGR 71 1 STITHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR

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                                                                                                                                                                                                                                                                                                                                                                                                               GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase (Fuc-T) is encoded by cDNA (AAQ98461) isolated from a human epidermal carcinoma cell line. The enzyme is responsible for the synthesis of 2'-fucosyllactose, one of the oligosaccharides in human milk. Other products of Fuc-T include glucoprotiens contq. beta-linked terminal galactose residues which can be fucosylated by Fuc-T. This DNA can be used to produce non-human transgenic mammals able to produce secondary gene products, e.g. oligosaccharides, in their milk. The transgenic mammals milk biochemically resembles human milk. This humanised milk can be used in the prepn. of an enteral nutritional product useful in the nutritive maintenance of an animal.
                       NALAPIFRISLPVLHSDIAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 149
                                    GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
                                                                    RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNWKGVVA 207
                                                                                                                              IQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
                                                                                                                                                                                                                                                                                                                                                                                 GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase; Fuc-T; synthesis; 2'-fucosyllactose; oligosaccharide; human milk; non-human transgenic mammal; secondary gene product.
                                                                                                               DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inserting heterologous gene encoding human catalytic entity which produces oligo:saccharide(s) and glyco:conjugate(s) into mammal's
                                                                                                                                                                                                                                                                                                                                                           GDP-L-fucose-beta-D-galactosidase alpha-1,2-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prodn. of human:ised milk by non-human transgenic mammal - by inserting heterologous gene encoding human catalytic entity wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ', Moreman KW, Mukerji P;
Smith DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 62-64; 83pp; English.
                                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                        AAR80154 standard; Protein; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US00926
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                                                                                                                                                                                                                                                                                                                                      (first entry)
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Prieto PA, Sn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-336739/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ABBO ) ABBOTT LAB.
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|PLWTLAKP 365
                                                                                                                                                                                                          PLLKALTP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ98461
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9524494-A1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JAN-1995;
                                                                                                                                                                                                                                                                                                                                      25-JUN-1996
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AAR80154
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                                                                                                                                                                                                                                                                                                                                                                                                          TOCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
                                                                                                        6,8
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New transgenic non-human mammal milk prods - contg. heterologous components produced as secondary gene prods. of an heterologous gene
                                                                                                    30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASME
                                                                                                                                                                                                                                              RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA
                                                                                                                                                                                                                                                                                                                                        GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase; glycosyltransferase; glycosylation; oligosaccharide; glycoprotein; glycolipid; transgenic animal; cattle; milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2-Alpha-fucosyltransferase (AAR70422) is encoded by a cDNA clone (AAT01083) isolated from a human epidermal carcinôma A431 library. The enzyme can be expressed in the milk of a transgenic mammal, esp. cow. This allows large-scale prodn. of oligosaccharides and
                                                                                                                                                                                                                                                                                                                  DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
                                      DB 16; Length 365;
                                                                       73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moremen KW, Mukerji P;
                               54.7%; Score 1051.5; DB 1063.3%; Pred. No. 4.3e-106; iive 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New transgenic non-human mammal milk prods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 62-64; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR70422 standard; Protein; 365 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-328284/42.
                                                 Similarity
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365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLLKALTP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLWTLAKP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT01083.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-1994;
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                                                                   195;
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Sequence
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                                  Query Match
                                                                   Matches
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                                                                                                                                                                                                                                                                               178
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                                                                                                       59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
                                                                                                                                                                           150 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 207
                                                                                                                                                                                        267
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                                                                                                                                                                                                                                                                       327
                                                                                                                                                                                                                                                                               118 AALAPVFRITLPVLAPEVDSRTPWRELQLHDWMSEEYADLRDPFLKLSGFPCSWTFFHHL 177
                                                                   Gaps
                                                                                     30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha-1,2-fucosyltransferase (AAR70421) is encoded by a cDNA clone
                                                                                                                                                                                                                                     TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS
                                                                                                                                                                                                                        DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
                                           54.7%; Score 1051.5; DB 16; Length 365; 63.3%; Pred. No. 4.3e-106; 1ve 37; Mismatches 73; Indels 3;
                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase; glycosyltransferase; oligosaccharide; glycoprotein; glycolipid; transgenic animal; cattle; glycosylation; milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic animal expressing heterologous catalyst - used in metabolite prodn esp. glycosyltransferase for prodn. of oligosaccharide(s) and glyco-conjugate(s) in the milk, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ď.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mukerji
 glycosylated proteins and lipids in the milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cummings RD, Kopchik JJ, Moremen KW,
Pierce JM, Prieto PA, Smith DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62-64; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         AAR70421 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-US01147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  foods, pharmaceuticals, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0209132
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2-Alpha-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-328279/42.
N-PSDB; AAT01082.
                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT LAB.
                       365 AA;
                                                                                                                                                                                                                                                                                                                PLLKALTP 335
                                                                                                                                                                                                                                                                                                                                     PLWTLAKP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     27-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9524488-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-1995.
                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                AAR70421;
                                           Query Match
                                                      Best Local
                                                                                                                                                                                                                        208
                                                                                                                                                                                                                                             238
                                                                                                                                                                                                                                                                    268
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SXS
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90 NALAPIFRISLPYLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 149
                                                                                                                                                                                    GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
                                                                                                                                                                                                                                              RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 207
                                                                                                                                                                                                                                                                                                                                                    DRGYLEKALDMFRARYSSPVFVVISNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL 267
                                                                                                                                                                                                                                                                                                                                                                                                                TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                 30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89
(AAT01082) isolated from a human epidermal carcinoma cell line A431 cDNA library. The enzyme can be expressed in the milk of a transgenic mammal, esp. cow. This allows large-scale prodn. of oligosaccharides or glycosylated proteins and lipids in the milk.
                                                                                                                                                                                                                                                                                                                                                                      Redn. of rejection of xenogeneic cells following transplantation by introducing a vector expressing fucosyl:transferase into the cells
                                                                                                                                          ..
m
                                                                                                          DB 16; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H-transferase; xenograft hyperacute rejection; transplantation; glycosyltransferase; galactose alpha(1,3) galactose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sandrin MS, Squinto SP;
                                                                                                                                        73; Indels
                                                                                                       54.7%; Score 1051.5; DB 16
63.3%; Pred. No. 4.3e-106;
iive 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rother RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 45-47; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0278282.
94US-0260201.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fodor WL, Mckenzie IFC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AUST-) AUSTIN RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human H-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-049326/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR90572 standard;
                                                                                                                       Similarity
                                                                           365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLLKALTP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLWILAKP 365
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15-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-DEC-1995.
                                                                                                                       Best Local Sim
Matches 195;
                                                                            Seguence
                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                       DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL 267
             The human H-transferase (AAR90572) product of a cDNA clone (AAT12238) prepd. from human epidermoid carcinoma cells (AIGC CRL 155 A-431) can be expressed in xenogeneic organs, tissues and cells using a vector such as pAPEX-1 (AAT12239). This results in decreased expression of the non-human antigen galactose alpha(1,3) galactose non the surface of the organs etc. so that hyperacute rejection is reduced upon transplantation to humans.
                                                                                                                                                                                                                                                                                                                            150 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 207
                                                                                                                                                                                                                                                                                                                                             TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                        59 GTAMGPNASSSCPOH-PASLSGTWTVYPNGRFGNOMGQXATLLALAQLNGRRAFILPAMH 117
                                                                                                                                                                                                             30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase;
                                                                                                                                                                                      3;
                                                                                                                                                            Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha 1,2 FT; transgene; transgenic mouse; animal model; intestinal adhesion; Helicobacter pylori infection; stomach; small intestine; gut; peithelial cell; surface receptor; carbohydrate antigen; gastritis; peptic ulcer; neoplasia; gastric adenocarcinoma; Lewis antigen; fucosylation.
                                                                                                                                                                                     73; Indels
                                                                                                                                                         Score 1051.5; DB 17;
Pred. No. 4.3e-106;
7; Mismatches 73; II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human alpha 1,2 fucosyltransferase (EC 2.4.1.69).
                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW23805 standard; Protein; 365
                                                                                                                                                         54.78;
63.38;
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                                                                                                                                                                   Best Local Similarity 63.39
Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-258275/23.
N-PSDB; AAT76768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gordon JI;
                                                                                                                            365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLWTLAKP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLLKALTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5625124-A.
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                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW23805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Falk P,
                                                                                                                                                                                                                                                                                                                                                       178
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A claimed transgenic mouse expresses, in its intestinal epithelial cells, the enzyme human GDP-L-fucose.beta-D-galactoside 2-alpha-L-fucosyltransferase (also called alpha 1,2 FT) or human GDP-L-fucose.beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase (also called alpha 1,3/4 FT). The enzyme is expressed under the control of a gut epithelial cell-specific promoter and Helicobacter pylori adheres to the transgenic cells. The transgenic mouse and intestinal epithelial cells from it are useful as models for screening compounds for the ability to inhibit adhesion of H. pylori to gut epithelial cells. The present sequence represents human alpha 1,2 FT and was published by Larsen et al., Proc.Natl.Acad.Sci.USA, 87:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
                                                                                                                                                                                                                                                                                                                                                                                                90 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207
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                                                                                                                                                                                                                                                                                                                                                                               89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 TQCNHTIMTIGTEGEWAAYLAGGDIVYLANFTLPDSEFLKIFKPEAAFLPEWGINADLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWGIPADLS
                                                                                                                                                                                                                                                                                                                       DB 18; Length 365;
            Helicobacter pylori infection - comprising expressing human enzyme promoting intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha(1,2)-fucosyltransferase; glycosylation; oligosaccharide;
                                                                                                                                                                                                                                                                                                                                                    73; Indels
                                                                                                                                                                                                                                                                                                                   54.7%; Score 1051.5; DB 18 63.3%; Pred. No. 4.3e-106;
                                                                                                                                                                                                                                                                                                                            63.3%; Pred. no.
                                                                  Example 1; Columns 13-16; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human alpha(1,2)-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW13640 standard; Protein; 365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US13816
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                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                       365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 PLLKALIP 335
            Animal model for
                           ransgenic mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLWTLAKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                              195;
                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW13640;
                                          adhesion
                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                               Matches
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Human GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase (AAW13640) is an enzyme involved in the expression of type I and II blood group in structures. Its amino acid sequence was deduced from an isolated DNA (AAT61677) derived from human A431 cells. Expression of the fucosyltransferase animal cell lines provides specific capabilities with respect to post-translational modification of the oligosaccharides of expressed proteins or lipids. Specific applas. Of the enzyme include enzymatic fucosylation of chain-terminating galactose residues on lactoseamine or neolacto type beta-D-galactoside to alpha-2-fucose residues. The enzyme can also be used to raise antibodies as diagnostic reagents and to screen cpds. for fucosyltransferase inhibitor activity.
                                                                                                                                                         New recombinant fucosyltransferase proteins - useful for modifying cell surface oligosaccharide structures
                                                                                                                                                                                                                 Example 1; Page 280-281; 329pp; English.
                  (UNMI ) UNIV MICHIGAN.
                                                            Lowe JB;
                                                                                               WPI; 1997-192897/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 AA;
                                                                                                                    N-PSDB; AAT61677
                                                        Legault DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Query Match 54.7%; Score 1051.5; DB 18; Length 365; Best Local Similarity 63.3%; Pred. No. 4.3e-106; Matches 195; Conservative 37; Mismatches 73; Indels 3;

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90 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 149 30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89 pp δÿ g

DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL 267 208

150 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 207

Óλ q Qy Db  $\Omega Y$ ΩD

268 TOCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWYGIPADLS 327 

328 PLLKALTP 335

358 PLWTLAKP 365

Search completed: May 27, 2003, 15:06:15 Job time: 46.4049 secs

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PDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 358
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US-09-298-886-8
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Listing first 45 summaries
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    protein search, using sw model

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                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09298886

Patent No. 6329170

GENERAL INFORMATION:
APPLICANT: Exic H. Holmes et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: THERROF

TITLE OF INVENTION: THERROF

FILE REFERENCE: 8511-029

CURRENT APPLICATION NUMBER: US/09/298,886

CURRENT FILING DAIE: 1999-04-26

NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                     Sequence 6, P
Sequence 3, P
Sequence 4, P
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Pred. No. 8.7e-214;
           US-08-539-005-33
US-09-280-598-35
US-09-390-111-5
US-07-906-349A-6
US-08-220-151-22
US-08-413-118-22
US-08-473-446-22
5470718-3
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US-08-208-887A-6
US-08-315-176-3
US-08-815-176-3
US-08-815-176-4
US-08-815-176-4
US-09-117-348-6
US-09-197-344-3
US-09-197-344-4
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Mismatches
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US-09-298-886-8
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Matches 358; Conserv
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SEQ ID NO 7
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      Sequence 10, Application US/09298886
Patent No. 6329170
GENERAL INFORMATION:
TITLE OF INVENTION: MUCLEIC ACIDS AND PROTEINS OF A RAT GANGLICSIDE
TITLE OF INVENTION: MUCLEIC ACIDS AND PROTEINS OF A RAT GANGLICSIDE
TITLE OF INVENTION: MUCLEIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE PATENTING DATE: 1999-04-26
SEQ ID NO: 29
SEQ ID NO: 25
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GENERAL INFORMATION:
APPLICANT: SANDRIM, MAURO S.
APPLICANT: SANDRIM, MAURO S.
TITLE OF INVENTION: NOCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.505W0
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT APPLICATION NUMBER: PCT/AU97/00540
PRIOR APPLICATION NUMBER: PC 1999-06-11
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-23
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
FENGENT : 2.0
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100.0%; Pred. No. 6.1e-211;
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Pred. No. 2e-159;
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81.9%;
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ORGANISM: Sus scrofa
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Best Local Similarity
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US-09-298-886-10
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Best Local S
Matches 353
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STIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
                                  Gaps
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APPLICANT: SANDELM, MAURO S.
APPLICANT: MCENZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
TITLE OF INVENTION: NUMBER: US/09/254,077A
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR PAPLICATION NUMBER: FCT/AUG97/00540
PRIOR PILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: PO 1823
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
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81.9%; Pred. No. 2e-159;
live 26; Mismatches 2
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Best Local Similarity 79.2 Matches 262; Conservative
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US-09-254-077A-8
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2-ALPHA-L-FUCOSYLTRANSFERASES, DNA SEQUENCES ENCODING THE
SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
GENOTYPING A PERSON
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                                                                                                                                                                                                                                                                                                                   SINGESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 STATE: VIRGINIA STOUTHY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPRINING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                 309 PDSPFLKLFKPEAAFLPEWIGIEADLSPLLK 339
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C8/395,800A
FILING DATE: 28-FEB 1995
CLASSIFICATION: 435
TELECOMMUNICATION: 135
TELEPHONE: (703) 413-220
TELER: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TENTH: 343 amino acids
              PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                             Sequence 8, Application US/08395800A Patent No. 5807732
                                                                                                                                                                                                                APPLICANT: ROUQUIER, SYLVIE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B
APPLICANT: LENNON, GREGORY
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Best Local Similarity 79.2's
Matches 262; Conservative
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TITLE OF INVENTION: 2-A
TITLE OF INVENTION: SAM
TITLE OF INVENTION: GEN
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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US-08-395-800A-8
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US-08-395-800A-8
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Patent No. 6329170
GENERAL INFORMATION:
APPLICANT: Eric H Holmes et al.
TITLE OF INVENTION: MUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE OF INVENTION: UMBER: US/09/298,886
CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: SANDRIN, MAURO S.
APPLICANT: SANDRIN, MAURO S.
TITLE OF INVERNICH: IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.50SMO
CORRENT APPLICATION NUMBER: US/09/254,077A
CURRENT PILING DATE: 1999-06-11
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1996-08-23
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 STIFHVQQRLAKIQAM--WELPV------QIPVLASTSKALGPSQLRGMWTINAIGR
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                                                    PDSPFLKIFKPEAAFLPEWTGIAADLSPLLK 342
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PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                                                                                              Sequence 8, Application US/09254077A Patent No. 6399758
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PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
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PCT-US91-00899-11
Sequence 11, Application PC/TUS9100899
SGREAL INFORMATION:
APPLICANT: Lowe, John B.
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Best Local Similarity
Matches 206; Conserv
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APPLICANT: SANDEIN, MAURO S.
APPLICANT: SANDEIN, MAURO S.
TITLE OF INFORMATION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562 505W0
CURRENT APPLICATION NUMBER: 05/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-11
PRIOR PLICATION NUMBER: PCT/AU97/00540
PRIOR PLICATION NUMBER: PCT/AU97/00540
PRIOR FILING DATE: 1996-08-23
PRIOR FILING DATE: 1996-08-23
SOFTWARE: PALENTIN VOX: 12
SOFTWARE: PALENTIN VOX: 2.1
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                                                                                                                                                                                                                                                                                                                                                                   ENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGIFGIWAAYLAGGDTIYLANYT 299
                                                                                                                                                                                                                                                                                                                                                                                                252 ENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LGNQMGEXATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                 121 WMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGS 179
                                                                                                                                                                                                                                                              180 QPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCR 239
                                                                                                                                                                                                                                                                                                                        LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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                                                                                                                                         23 STIFHVQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGMWTINAIGR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.7%; Score 1396.5; DB 4; Length 347; 79.2%; Pred. No. 4.3e-153;
                                                            Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                           Indels
                                                                                         32;
                                                           72.7%; Score 1397; DB 4; 78.9%; Pred. No. 3.7e-153;
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                                                                                        26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              300 LPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09254077A Patent No. 6399758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262; Conservative
                                                                                         Conservative
              ; ORGANISM: Homo sapiens US-09-298-886-11
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                                                                           Similarity
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                                                                                         262;
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TITLE OF INVENTION: Wethod and Products For the synthesis of TYPLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids, TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned TITLE OF INVENTION: Genetic Sequences That Determine These Structur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 SEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISL 100
                                241 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHIIMTIGTFGIWAAYLAGGDTIYLANYTL 300
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                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: SANDRIN, MAURO S.
TITLE OF INVENTION: WCENELLE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.505W0
CURRENT APPLICATION NUMBER: 0X/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-12
PRIOR PLICATION NUMBER: PCI/A097/00540
PRIOR PLICATION NUMBER: PO 1823
PRIOR PLILNG DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 FRARHEAPIFVVTSNGMKWCWENIDASRGDVVFAGNGLESSPAKDFALLTQCNHTVMTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 SFLLHLHQDLFRNGLALSLPCLERQPVPAPVAIVCLPVTSPASNASSCAGRPAAPS----
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Pred. No. 4.5e-
50; Mismatches
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METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISCLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
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                                                                                                                       ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor
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                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/914,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11arity 63.3%; Score 1051.5; DB 1; Score 1051.5; DB 1; Conservative 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2363-060-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Lavallaye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-066
                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08393246
Patent No. 5595900
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 365 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
TITLE OF INVENTION: METITIED OF INVENTION: OF GLY TITLE OF INVENTION: OF NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 195; Conserv
                                                                                                                                                                                   CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                U.S.A.
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CLASSIFICATION:
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                                                                                                                                                                                                                                                 22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 333;
              CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73; Indels
                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCI/US91/00899 FILING DATE: 19910214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.7%; Score 1051.5; DB 5;
63.3%; Pred. No. 3.7e-113;
Live 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye Ph.D., Jean-Paul
REGISTRATION NOMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-021-55 PC:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-5940
TELEPAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                           PC-DOS/MS-DOS
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; Sequence 6, Application US/07914281
; Patent No. 5324663
; GENERAL INFORMATION:
                                                                                                                                                                            MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 333 amino acids
AMINO ACID
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                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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NUMBER OF SEQUENCES:
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                                                                                                CITY: Arlington STATE: Virginia ZIP: 22202
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                                                                                                                                                                                                                                                                                                    FILING DATE: 19
CLASSIFICATION:
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MOLECULE TYPE:
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ADDRESSEE:
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                    OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89
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                                                                                                                      OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT.
P.C.
                                                                                                                                                     l: 1755 Jefferson Davis Highway, Fourth Floor
Arlington
                                                                                                                                                                                                                                                                                                                          SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.7%; Score 1051.5; DB 1; 63.3%; Pred. No. 4.3e-113; tive 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 2363-060-55 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
AMME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,246
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31,451
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TELEFAX: (703)486-2347
TELES: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
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TITLE OF INVENTION: METHILLE OF INVENTION: OF CITTLE OF INVENTION: GLY UNDERROOF SEQUENCES: 14 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) MOLECULE TYPE: protein US-08-393-246-6
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                     Virginia
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                                                                                                                      ADDRESSEE:
ADDRESSEE:
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RESULT 13

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"GDP-L-fucose:beta-D-Galactoside-2-alpha-L-fucosyl
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                                                                                                                 for Gastro-Intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 365
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.7%; Score 1051.5; DB 1 63.3%; Pred. No. 4.3e-113; ive 37; Mismatches 73;
                                                                                                                                                                                                     :: Patrea L. Pabst
1100 Peachtree Street, Suite 2800
Sequence 1, Application US/08273411
Patent No. 5655124
GENERAL INFORMATION:
APPLICANT: Falk, Per
APPLICANT: Gordon, Jeffrey I.
ITTLE OF INVENTION: Animal Model for ITTLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERRACE/DOCKET NUMBER: WUITELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31,284
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Proc. Nat'l Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                         ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: 1..365 OTHER INFORMATION: /not PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 195; Conservative
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linear
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                   Atlanta
                                                                                                                                                                                                                                                                                               USA
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GENERAL INFORMATION:

APPLICANT: LOWE, JOHN B

APPLICANT: LOWE, JOHN B

APPLICANT: LOWE, JOHN B

APPLICANT: ROUGHIER, SYLVIE

APPLICANT: GIORGI, DOMINIQUE

APPLICANT: GIORGI, DOMINIQUE

APPLICANT: GELLY, ROBERT J

TITLE OF INVENTION: 2-ALPHA-L-FUCOSF: BETA-D-GALACTOSIDE

TITLE OF INVENTION: GENOTYPIA PERSON

TITLE OF INVENTION: GENOTYPING A PERSON

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
                                           TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPELCATION NUMBER: US/08/395,800A FILING DATE: 28-FEB-1995 CLASSIFICATION: 435 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                           Sequence 6, Application US/08395800A Patent No. 5807732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703) 413-3000
(703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 365 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALINGTON STATE: VIP
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Best Local Similarity
                                                                                                      PLLKALTP 335
                                                                                                                                           358 PLWTLAKP 365
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TELEFAX: (
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                      268
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                                                                                                                                                                                                                                                                                                                  APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
CORRESPONDENCE ADDRESS:
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                                     268 TQCNHTIMTIGTFGIWAAXLAGGDTIXLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS
                                                          DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
238 DSAYLRQAMDWFRARHEAPVFVVTSNGMEWCKENIDTSQGDVTFAGDGQEATPWKDFALL
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1755 Jefferson Davis Highway, Fourth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/525,058A
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63.3%; Pred. No. 4.3e-113;
tive 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGRWT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            Sequence 6, Application US/08525058A Patent No. 5770420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMONICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT INFORMATION FOR SEQ ID NO: 6:
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amino acid
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Best Local Similarity 63.34
Matches 195; Conservative
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MEDIUM TYPE: Floppy
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Search completed: May 27, 2003, 15:11:51 Job time: 15.7192 secs
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May 27, 2003, 15:08:29 ; Search time 15.4676 Seconds (without alignments) 2295.367 Million cell updates/sec
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3. /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

4. /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

5. /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

6. /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

7. /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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10. /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

11. /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

12. /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

13. /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

14. /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

13. /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum DB seq length: 200000000
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | Description                | Sequence 8, Appli<br>Sequence 10, Appli<br>Sequence 10, Appli<br>Sequence 11, Appli<br>Sequence 11, Appli<br>Sequence 11, Appli<br>Sequence 10, Appli<br>Sequence 4, Appli<br>Sequence 13, Appli<br>Sequence 13, Appli<br>Sequence 2, Appli<br>Sequence 29, Appli<br>Sequence 29, Appli<br>Sequence 29, Appli<br>Sequence 647, Appli<br>Sequence 647, Appli<br>Sequence 647, Appli<br>Sequence 647, Appli  |
|-----------|----------------------------|--|
|           | QI                         | US-09-999-672-8<br>US-10-040-863-8<br>US-09-999-672-10<br>US-10-040-863-10<br>US-09-999-672-11<br>US-10-10-863-11<br>US-10-105-963-11<br>US-10-105-963-11<br>US-09-863-475A-6<br>US-09-864-268-13<br>US-09-844-75-13<br>US-09-848-838-2<br>US-09-479-614-14<br>US-09-479-614-25<br>US-09-479-614-29<br>US-09-479-614-29<br>US-09-479-614-29<br>US-09-479-614-29<br>US-09-479-614-29<br>US-09-479-614-29<br>US-09-479-614-29<br>US-09-479-614-29<br>US-09-479-614-29<br>US-09-479-614-29  |
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|           | Score                      | 1921<br>1981<br>1896<br>1886<br>1886<br>1081<br>1081<br>1081<br>1081<br>1081<br>108  |
|           | Result<br>No.              | 11111111111111111111111111111111111111   |

| Sequence 17, Appl<br>Sequence 6, Appli<br>Sequence 1, Appli |                                | equence 213                    | equence 212      | 213              | equence 217      | equence 21       | equence 21       | ednence 717      | ednence ZI       | equence 21.      | ednence 21.      | ednence 71       | ednence 71       | 77               | 7                | Sequence ZIZ, App | 21              | Sequence 212, App | Sequence 212, App |          |
|---|--------------------------------|--------------------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-------------------|-----------------|-------------------|-------------------|----------|
| US-09-815-379-1<br>US-09-765-298A<br>US-10-235-521-1        | 09-895-913A-5<br>-09-815-242-1 | US-10-028-072<br>US-10-121-049 | US-10-140-470-21 | US-10-175-746-21 | US-10-176-921-21 | US-10-137-865-21 | US-10-140-474-21 | US-10-142-431-21 | US-10-143-114-21 | US-10-140-002-21 | US-10-142-419-21 | US-10-123-262-21 | US-10-142-423-21 | US-10-121-050-21 | US-10-141-755-21 | US-10-143-032-21  | US-10-123-108-2 | US-10-123-236-21  | us-10-123-261-21  |          |
| 2058 9<br>217 1<br>738 9                                    |                                |                                |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                  |                   |                 |                   |                   |          |
| 444<br>6.5.0  |                                | 4 4 .<br>v. v. c               | 4. 4.<br>J. W.   | 4. A             | 4.3              | 4.3              | 4.3              | 4.3              | 4.3              | 4.3              | •                | •                | 4.3              | 4.3              |                  | 4.3               |                 |                   |                   |          |
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## ALIGNMENTS

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Sequence 8, Application US/0999672;
Sequence 8, Application US/0999672;
Patent No. US20020127655A1
GENERAL INFORMATION:
APPLICANT: EILC H. HOLMES et al.
TITLE OF INVENTION: MULLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES;
TITLE OF INVENTION: THEREOF;
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT FILING DATE: 2001-10-31
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOGTWARR: PATENTIN NOS: 29
COTTON OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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Best Local Similarity 100.0%; Score 1921; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.7e-190;
Matches 358; Conservative 0; Mismatches 0; 1
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RESULT 1
US-09-999-672-8
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Sequence 10, Application US/09999672

Sequence 10, Application US/09999672

Patent No. US20020127655A1

GENERAL INFORMATION:

APPLICANT: ETIC H. HOLMES et al.

APPLICANT: ETIC P. INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 8511-029

CURRENT APPLICATION UNMBER: US/09/599,672

CURRENT FILING DATE: 2001-10-31

PRIOR APPLICATION NUMBER: US/09/298,886
241 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ELTERATION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE TITLE OF INVENTION: OMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES TITLE OF INVENTION: THEREOF FILE OF INVENTION: THEREOF FILE OF INVENTION: THEREOF FILE OF INVERSE SOLIDIOS OF SOLIDIOS 
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Pred. No. 1.7e-190;
Mismatches 0;
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Patent No. US20020137165A1
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Best Local Simi
Matches 358;
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61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIFNQNYHLNDMMEER 120
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APPLICANT: Eric H. Holmes et al.

APPLICANT: Eric H. Holmes et al.

ITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE

TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES

TITLE OF INVENTION: THEREOF

FILE REPERENCE: 8511-029

CURRENT APPLICATION NUMBER: US/10/040,863

CURRENT FILING DATE: 2001-11-01

PRIOR PILING DATE: 1999-04-23

NUMBER OF SEQ ID NOS: 29
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Pred. No. 5.8e-188;
0; Mismatches 0;
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Pred. No. 5.8e-188;
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Patent No. US20020137165A1
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Best Local Similarity 100.0%; Pr
Matches 353; Conservative 0;
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US-10-040-863-10
                                                                                                                                            ; ORGANISM: Rattus norvegicus
US-09-999-672-10
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
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SEQ ID NO 11
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WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
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APPLICANT: MCKENZIE, IAN FARQUHAR CAMPBELL
APPLICANT: ASANDRIU. MAURO SERGIO
TITLE OF INVENTION: MCROUSED NUCLEIC ACIDS ENCODING A CHIMERIC
FILE REFERENCE: 30562.60SWO
CURRENT APPLICATION NUMBER: US/09/051,034A
CURRENT FILING DATE: 1998-03-31
PRIOR PLING DATE: 1998-03-1
PRIOR APPLICATION NUMBER: 60/024,279
PRIOR FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: 60/024,279
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
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81.9%; Pred. No. 6.9e-142;
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US-09-051-034A-2
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Best Local Similarity
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US-09-051-034A-2
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RESULT 6 US-09-999-672-11

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APPLICANT: Exic H. Holmes et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GAI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERAŜE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US/09/298,886
PRIOR APPLICATION NUMBER: US/09/298,886
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Patent No. US20020137165A1
GENERAL INFORMATION:
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: UNCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GM-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THERROF
FILE REPERENCE: 8511029
CURRENT APPLICATION NUMBER: US/10/040,863
CURRENT APPLICATION NUMBER: 09/298,886
PRIOR APPLICATION NUMBER: 09/298,886
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 STIFHVOORLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGMWTINAIGR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 STIIHLQORIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 344;
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Pred. No. 2.8e-136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 72.7%; Score 1397; DB 10; Best Local Similarity 78.9%; Pred. No. 2.8e-136; Matches 262; Conservative 26; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 LPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
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Sequence 11, Application US/0999672 Patent No. US20020127655A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.78;
78.98;
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-672-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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Best Local Similarity
                                                    GENERAL INFORMATION:
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TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARLDS STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
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30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.7%; Score 1051.5; DB 1
63.3%; Pred. No. 1.9e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/863,475A FILING DATE: 24-May-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/914,281 FILING DATE: 20-JUL-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lavalleye, Jean-Paul M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
                                                                                                                                                                                            Sequence 6, Application US/09863475A Patent No. US20020102688A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                        APPLICANT: LOWE, JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Virginia
                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                       PLLKALTP 335
                                                                                             PLWILAKP 365
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Publication No. US20030068818A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Glark, J. Michael
TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
FILE OF INVENTION: Recombination
FILE OF INVENTION: Recombination
FILE REPERENCE: 731/002
CURRENT APPLICATION NUMBER: US/10/105,963
CURRENT FILING DATE: 2002-03-21
PRIOR FILING DATE: 2001-03-21
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                                                                                                                                                                                              121 WMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGS 179
                                                                                                                                                                                                                     QPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCR 239
                                                                                                                                                                                                                                                                                               LGNOMGEYATLFALARMNGREAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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                                       STIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
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32;
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26;
                                                                          STIFHVQQRLAKIQAM--WELPV---
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SOFTWARE: Patentin versic
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT CAGANISM: Homo sapiens US-10-105-963-10
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US-10-105-963-10
262;
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                                                       NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS 259
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51 PVAIFCLAGTPVHPNASDSCPKH-PASFSGTWTIYPDGRFGNQMGQYATLLALAQLNGRQ 109
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Patent No. US20010055584A1

APPLICANT: MCKENIE, IAN FARQUHAR CAMPBELL

APPLICANT: SANDRIN, MAURO SERGIO

TILLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC

TILLE OF INVENTION: IMPROVED NUCLEIC ACIDS

FILE REPERBRACE: 30562.6USWO

CURRENT APPLICATION NUMBER: US/09/051,034A

CURRENT APPLICATION NUMBER: BCT/AU97/00492

PRIOR APPLICATION NUMBER: 60/024,279

PRIOR PILING DATE: 1997-08-01

PRIOR PILING DATE: 1996-08-21

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 4

LENGTH: 365
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; Patent No. US20020129395A1
; GENERAL INFORMATION:
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APPLICANT: BOSWORTH, BRAD

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APPLICANT: VOGELI, PETER
TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
TITLE OF INVENTION: RESISTANT TO F18 E. COLI ASSOCIATED DISEASES
FILE REPERENCE: 21419/90368
CURRENT APPLICATION NUMBER: US/09/844,268
CURRENT FILING DATE: 2001-04-27
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATCHIIN VOET: 2.0
SOFTWARE: PATCHIIN VOET: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 PMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 PMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRL 81
                                                                                                                                                                                                                                                                                                                                                               Length 365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VOGELI, PETER
TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY
TITLE OF INVENTION: RESISTANT TO F18 E. COLI ASSOCIATED
FILE REPERENCE: 21419/90368
CURRENT APPLICATION NUMBER: US/09/844,705
CURRENT APPLICATION NUMBER: 09/443,766
PRIOR APPLICATION TO TUBER: 09/443,766
PRIOR FILING DATE: 1999-11-19
                                                                                                                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                               54.4%; Score 1044.5; Di
62.6%; Pred. No. 1e-99;
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Patent No. US20020138386A1
GENERAL INFORMATION:
APPLICANT: BOSWORTH, BRAD
                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
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US-09-844-705-13
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Matches 194;
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51 PVAIFCLAGTPVHPNASDSCPKH-PASFSGTWTIYPDGRFGNQMGQYATLLALAQLNGRQ 109
                                  82 AFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPC 141
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APPLICANT: TAYLOY, Diane
APPLICANT: TAYLOY, Diane
APPLICANT: Wang, GE
APPLICANT: Palcic, Monica
ITLLE OF INVENTION: ALPHA 1,2-FUCOSYLTRANSFERASE
FILE REFERENCE: 07254-061002
CURRENT FAPLICATION NUMBER: US/09/848,838
CURRENT FILING DATE: 12001-05-03
PRIOR PLING DATE: 1999-11-02
PRIOR PLING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 23
SOFTWRE: FASLEQ for Windows Version 4.0
SEQ ID NO 2
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Patent No. US20020037570A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT; ORGANISM: Helicobacter pylori
US-09-848-838-2
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Best Local Similarity 24.03
Matches 81; Conservative
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US-09-848-838-2
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APPLICANT: WECAL. Exic
APPLICANT: Weber, Exic
APPLICANT: Weber, Exic
APPLICANT: Weber, Exic
APPLICANTON: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT APPLICATION NUMBER: 60/115,033
EARLIER APPLICATION NUMBER: 60/115,033
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN USE: 2.0
                                                                                                                                                                                                                          APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Yang, Yong-Min
APPLICANT: Barankiewicz, Theresa J.
APPLICANT: Barankiewicz, Theresa J.
APPLICANT: Chen, Zhong
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: 2010/10.1.2,1
CURRENT FILING DATE: 2002-08-08
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.1
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      --- ESHFEVKSQ 296
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Pred. No. 0.14;
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; Sequence 14, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
                                                                                                        US-10-214-524-25; Sequence 25, Application US/10214524; Publication No. US20030073142A1
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Best Local Similarity 25.0%;
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Matches 52; Conservative
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276 HENILCKEWVKI--
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Compugen Ltd.
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GenCore version
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T31916
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T32309
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1: pir1:*
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transforming prote probable myb-prote glycoprotein D pre fimbrilin precurso peptide synthetase hypothetical prote myosin X - human modular adaptor Gr acyl carrier prote procollagen-lysine growth factor rece growth factor rece NADH2 dehydrogenas glycoprotein D pre A56098
alpha(1.2)fucosyltransferase Sec2, long form - human
c;Species: Homo sapiens (man)
c;Species: Homo sapiens (man)
c;Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 21-Jul-2000
c;Accession: A56098
R;Kelly, R.J.; Rouquier, S.; Giorgi, D.; Lennon, G.G.; Lowe, J.B.
J. Biol. Chem. 270, 440-0449, 1995
A;Title: Sequence and expression of a candidate for the human Secretor blood tes with the non-Secretor phenotype. probable membrane 61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120 121 WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHYREEAQAFLRGLRVNGSQ 180 tes with the non-Secretor phenotype.

A;Reference number: A56098; MUID:95181460; PMID:7876235

A;Accession: A56098

A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-343 < KEL>
A;Cross-references: GB:U17894; NID:9687618; PIDN:AAC24453.1; PID:9687619
C;Genetics: 23 STIFHYQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGWWINAIGR 1 STIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 11; Length 343; A:Cross-references: GDB:120619; OMIM:182100 A:Map position: 19913.3-19913.3 C:Keywords: glycoprotein; Golgi apparatus; transmembrane protein Indels DB 2; 32; 73.3%; Score 1407.5; DB 2 79.2%; Pred. No. 3.3e-110; iive 26; Mismatches 32; ALIGNMENTS T19293 T04452 E85384 VGBEEA JN0920 S61964 AB2934 E98348 A59267 VGBEG3 A54688 T45082 T08679 S26050 Best\_Local Similarity 79.2 Matches 262; Conservative A; Gene: GDB: FUT2; SE Query Match 192 181 72 õ g δ g  $\Omega$ Db

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Gaps 9 240

251

NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300 

PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331

301 312

22 g ά RESULT 2

191

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PVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLH 160
                                                                                                        DHVREEAQAFIRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
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Matches 195; Conserv
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A;Molecule type: mRNA
A;Residues: 1-365 <LAR>
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            C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999
C.Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999
C.Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999
R.Hitcshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
J. Biol. Chem. 270, 8844-8850, 1995
A.Title: Molecular cloning and expression of two types of rabbit beta-galactoside alphal A.Reference number: A56392; MUID:95238380; PMID:7721792
A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rabbit beta-galactoside alpha
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C; Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999
C; Accession: A56392; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
J; Biol. Chem. 270, 8844-8850, 1995
A; Title: Molecular cloning and expression of two types of rabbit beta-galact A; Accession: A56392; MUID: 95238380; PMID: 7721792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 SEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GIWITHPDGRFGNQMGQYATLALAQLNGRRAFILPAMHAALAPVFRITL 128
                                                                                                                                                                                                                                                                                                                                                                                                                             38 STVFHCHORLAL-----VPAPWAYSARVVVVP-----GHLPREGMWTINAMGR 80
                                                                                                                                                                                                                                          A;Cross-references: GB:X80225; NID:g854356; PIDN:CAA56512.1; PID:g854357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB: X80226; NID: g854354; PIDN: CAA56513.1; PID: g854355
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                                                                                                                                                                                                                                                                                                                                               44; Indels
beta-galactoside alphal, 2-fucosyltransferase II - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             beta-galactoside alphal, 2-fucosyltransferase I - rabbit
                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                    67.5%; Score 1296.5; DB 2; 73.9%; Pred. No. 6.8e-101; tive 25; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.5%; Score 1086; DB 2;
58.7%; Pred. No. 3.1e-83;
Live 50; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDSPFLKVFKPEAAFLPEWVGIPADLSPLL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 73.9 Matches 244; Conservative
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A; Residues: 1-373 <HIT>
                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-354 <HIT>
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Best Local S
Matches 206
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CiAccession: A36047

Riarsen, R.D.; Ernst, L.K.; Nair, R.P.; Lowe, J.B.

Proc. Natl. Acad. Sci. U.S.A. 87, 6674-6678, 1990

A;Title: Molecular cloning, sequence, and expression of a human GDP-L-fucose:beta-D-g A;Accession: A36047; MUID:90370848; PMID:2118655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) B - rat (fragment) N;Alternate names: alpha-1,2-fucosyltransferase (Species: Rattus norvegicus (Norway rat) (Species: Rattus norvegicus (Norway rat) (Species: 26-Dec-1994 #sequence_revision 23-Feb-1996 #text_change 08-Oct-1999 (Shacession: S46494 R;Piau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G. Biochem. J. 300, 623-626, 1994
                                                                                                                                                                                                                                                                                                                                                                                             C.Species: Homo sapiens (man)
C.Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 10-Sep-1997
                               FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 AALAPVFRITLPVLAPEVDSRTPWRELQLHDWMSEEYADLRDPFLKLSGFPCSWTFFHHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.7%; Score 1051.5; DB 2; Length 365; 63.3%; Pred. No. 2.3e-80;
                                                                                                                          galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:M35531; NID:g183887; PID:g306830
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Gaps

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Aganonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 198
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Note: see websites genome wustl.edu/gsc/C_elegans/ and www_sanger ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Status: preliminary
A;Notecasion: H87911
A;Status: preliminary
A;Mossiques: 1-443 <STO>
A;Cross-references: GB:chr_I; PIDN:AAC16988.1); PID:g3150470; GSPDB:GNG0019; CESP:B020
                                                                                                                                           CyAccession: T44328
RYamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Gene 237, 321-332, 1999
A:Yitle: The genes responsible for O-antigen synthesis of Vibrio cholerae 0139 are classecsion: T44328
A:Reference number: 222749; MUID:99453293; PMID:10521656
A:Reference number: 222749; MUID:99453293; PMID:10521656
A:Reference number: 222749; MUID:99453293; PMID:10521656
A:Reference: Tall A:Reference: Tall A:Reference: BMBL:AB012957; NID:94115688; PIDN:BAA33632.1; PID:93721682
A:Experimental source: strain 022
A:Experimental source: strain 022
A:References: A:References: A:References: CyGenetics: CyGenetics: A:References: CyGenetics: CyGenetics
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                                                                                                                   21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 28-Jul-2000
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H87911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 MFTINSIGRLGNOMGEYATLFALARMNG---RL---AFIPASMHNALAPIFRISLPVLHS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFVGVHYRRGDYVHV 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSPAKDFALLTQCNHTIMTIGTFGIWAAYL-AGGDTIYLANYT------LPDS 303
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20.6%; Pred. No. 1.7e-07;
Live 53; Mismatches 128; Indels 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.2%; Score 214.5; DB 2; Length 281; llarity 26.5%; Pred. No. 2.1e-10; Conservative 50; Mismatches 102; Indels 67
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Best Local Similarity 20.64
Matches 72, Conservative
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hes 79; Conserv
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Matches
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A.Reference number: S46493; MUID:94280382; PMID:8016942
A.Accession: S46494
A.Molecule type: mRNA
A.Residenule type: mRNA
A.Residenule type: mRNA
A.CONTON A.BONTON A
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A; Molecule type: mRNA
A; Cross-references: EMBE:L26009; NID:9414814; PIDN:AAB41514.1; PID:9554438
B; Piau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
Biochem, J. 300, 623-626, 1994
A; Fitle: Evidence for two distinct alpha-(1,2)-fucosyltransferase genes differentially
A; Reference number: S46493; MUID:94280382; PMID:8010942
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C;Date: 07-May-1995 #sequence_revision 17-Nov-1995 #text_change 08-Oct-1999
C;Accession: S51582; S46403
R;Plau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
submitted to the EMBL Data Library, November 1993
A;Reference number: S51582
A;Accession: S51582
                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:L26010; NID:g414816; PIDN:AAB41515.1; PID:g414817 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 PCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVN--GSQPSTFVGVHVRRGDYVHV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 MPNVWKGYVADRGYLEKALDMFRARYSSPVFVVTSNCMAWCRENINASRGDVVFAGNGIE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein wblh [imported] - Vibrio cholerae C:Species: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 VGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 846; DB 2;
Pred. No. 1.3e-63;
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Pred. No. 1.8e-41;
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A; Residues: 9-135 <PI2>
A; Cross-references: EMBL:L26009
C; Keywords: glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: FTB
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Mismatches
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Best Local Similarity 99.4%;
Matches 158; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Caenorhabditis elegans and attaction 15-oct-1999 #text_change 20-Jun-2000 Accession: T20745
                                                                                                                                                                                                                                          QQISXIYENVAFIICSDNVAMARRNLKLGKETLHFF---CPGPREVDMAILKSCDSVIIS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 PSSVKRVKFHQKCCTFDDPSLLDNYEDEYLHLTG~---THYQ-SWKYFSHMRNELI--- 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257
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                                                                             DPVRKRVSFWNIIYWNIHPTNHRKKPEKSTVSIFSFVTFQLRVDEFLENVGISLTVRNAR 276
                                                                                                                         176 V-----NGSQ------PSTFVGVHVRRGDYVHV--MPNVWKGVVADRGYLEKAL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 TLHDHVREEAQAFLRGLRVNGSQPSTFVG-VHVRRGDYVHVMPNVWKGV-VADRGYLEKA 215
ASKITLTSCCAYRNLSTILFNDSRI-----IERIDGYFQNFRYFHPDSQKIVKKLFTFM 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGRLGNQMGEYATLFALARMNGRLA--FIPASMH-----NALAPIFRISLPVLHSDT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNLISRQVAKRANTAT-------VFFGDDYEFMDSLRNRTSKINAFVSQ
                                                                                                                                                      217 DMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 GSPAKDFALL-TQCNHTIMTI--GTFGIWAAYLAGGDTIYLANYTLPDSPFLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 42/1; 55/2; 136/3; 175/3; 210/2; 243/1; 299/1; 330/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 363;
                                                                                                                                                                                                                                                                                                                   IGTFGIWAAYL---AGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGI 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.9%; Score 170.5; DB 2; Length 3 Best Local Similarity 23.4%; Pred. No. 1.4e-06; Matches 73; Conservative 45; Mismatches 101; Indels
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hypothetical protein C17A2.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein FliA5.5 - Caenorhabditis elegans
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Molecule type: DNA
Residues: 1-363 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 VFKPEAAFLPEW 319
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                                          DHVREEAQAF
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A;Cross-references: EMBL:AF016654; PIDN:AAB66030.1; GSPDB:GN00020; CESP:C17A2.4
A;Experimental source: strain Bristol N2; clone C17A2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
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C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000 C;Accession: T31916  
R;Sammons, L.; Wohldmann, P. Asamons, L.; Wohldmann, P. Asbenitted to the EMBL Data Library, July 1997 A;Pescription: The sequence of C. elegans cosmid C17A2. A;Reference number: 221098 A;Reference number: 221098 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-348 <SAM>A;Residues: 1-348 <SAM>A;Resi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein K06H6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 TLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGV-VADRGYLEKAL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 SIGRLGNQMGEYATLFALARMNGR--LAFIPASMHNALAPIFRISLP-----VLHSDI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 AKKI---PWQ-----NYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 DMFRARYSSPV-----FVVTSNGMAWCR---EN--INASRGDVVFAGNGI--EGSPA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 SPSRLGNHIFEFASLFGLSERLHRTPLFLVENEFHQKMLDETRKVMPGLVEKFTVINGSL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 2
A;Introns: 94/3; 133/3; 168/2; 272/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
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R; David, M.; Wohldmann, P.; Bauer, C.; Clarke, K.
submitted to the EMBL Data Library, September 1997
A; Description: The sequence of C. elegans cosmid K06H6.
A; Reference number: Z21147
A; Accession: T32294
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ilarity 22.8%; Pred. No. 3.5e-05;
Conservative 50; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

8.0%; Score 154; DB 2; I
Best Local Similarity 22.8%; Pred. No. 3.3e-05;
Matches 63; Conservative 53; Mismatches 102;
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A; Experimental source: strain Bristol N2; clone K06H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-335 <DAV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| | | : :: | | | | : :: EDLTYSKQNCDIVLISAPKSTFGWWIGYFSKGNKVF 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDFALLTQ-CNHTIMTI--GTFGIWAAYLAGGDTIY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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A;Gene: CESP:K06H5.6
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Best Local Sim
Matches 77;
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28 09:23:04

Wed May

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304 PFLKVFKPEAAFLPEW 319
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                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
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A:Introns: 16/1; 51/3; 77/1; 131/3; 170/3; 209/2; 244/1; 269/1; 297/3; 324/1; 354/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-383 <WIL>
A;Cross-references: EMBL:299710; PIDN:CAB16868.1; GSPDB:GN00019; CESP:F08A8.5
A;Experimental source: clone F08A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
                                                                                                                -----NCDTVLITAPHSTFGWW 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 EIYRRMIESSKEAIPGLVGOFEILNG----KVPLYIKNIKLNIRCCVFVDPLIHEHNNDE 140
                                                                                                                                                                                                                        181 TSFVTCVHIRRGDFKRV-----GFAESDEWFIRKAKEFVENKEATSKPCSHVVLFGDDL 234
                                                                                                                                                                                                                                                                     235 --MAWCREN-----INASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTI--GTFGIW 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 --MEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVRE-EAQAFLRGLRVNG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---CNHTIMTI--GTFGIWAAYLAGGD-TIYLANYTLPDSPFLKVFKPEAA 314
  --- DWMEER 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 -------DIHFAYTVFEDRVAHFTFLOKPVNNSYDYSLPQISPSYTAILTPTL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 TPEIDLAFSRLFCOVTLITAPSSIFGWWLSYLAKRTATTYYRDILESKDGVAGEMHPEDF 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 QMSSGNTESPEMRRDSEQHGNGE--LRGMFTINSIGRLGNQMGEYATLFALARMNGRLAF 83
                                                                                       YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQP----
                                                                                                                                                                              182 STFVG-VHVRRGDYVHVMPNVWKGVV-ADRGYLEKALDMF--RARYSSPVFVVTSNG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 IPA-----SMHNALAPIFRISLPVLHSD-TAKKIP--WQNYHLNDW-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 GMAWCRENINASRGDVVFAGNGIEGSPAK---------------------ALLTQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.3%; Score 139.5; DB 2; Length 383; Best Local Similarity 21.7%; Pred. No. 0.00061; Matches 81; Conservative 52; Mismatches 135; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F08A8.5 - Caenorhabditis elegans
SMHNALAPIFRISLP-----VLHSDTAKKIPW--QNYHLN-
                                                                                                                                                                                                                                                                                                                                                                                        281 MGYFSKGDKVYYMDIRETRDNVYRNGGLNPYDYYLPHW 318
                                                                                                                                                                                                                                                                                                                                                            284 AAYLAGGDTIYLANY-TLPDSPFLK-VFKPEAAFLPEW 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rifarris, B. submitted to the EMBL Data Library, October 1997 submitted to the EMBL Data Library, October 1997 A.Accession: T20572 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: DNA
                                                                                                                                                                                                                                                                                                               235 PFMKNLYENESTHFVSVNSPSDDLVYAKN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : |||: : ||:
365 YPPEWIKLKTDLN 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP: F08A8.5
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                                       Db
                                                                                       QΫ
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Probable alpha(1,2)fucosyltransferase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000
C;Accession: H71976
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric p
A;Accession: H71976
A;Status: preliminary
A;Accession: H71976
A;Status: preliminary
A;Cross-references: GB:AE001447; GB:AE001439; NID:g4154583; PIDN:AAD05659.1; PID:q415
A;Esperimental source: strain J99
C;Genetics:
A;Gene: ihp0086
C;Superfamily: Vibrio cholerae hypothetical protein wbla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                          Rywhite, S.
Submitted to the EMBL Data Library, November 1996
A; Reference number: 219508
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-50C < MLL>
A; Cross-references: EMBL: 281537; PIDN: CAB04377.1; GSPDB: GN00019; CESP: F41D3.6
A; Experimental source: clone F41D3
hypothetical protein F41D3.6 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T22068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 EQVISVPIEPSETIRFAISSDCCRXELSDNHLAD--ESKFLVIEGHYFQ-----SYKYF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 KGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 ---ISLPVLHSDTAK-----KIPWQNYHLNDWMEERYRHIPGHFVRFIGYPCSWTFY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFALL-------TQCNHTIMTI--GTFGIWAAXLAGGDT-IYLANY-TLPDS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 HHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYV----HVMPNVW 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 ADMKLSI-KEWL----KPEDPEKFRMMISKIESQRHK-TCVHVRRGDFLTDEQH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --AGTDSNYTISAIDHLKSLYHGVIFIM-SNDPKWVKVHI-ADHLDY------QK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: CESP:F41D3.6
A;Map position: 1
A;Introns: 23/1; 59/1; 112/3; 150/3; 222/1; 278/1; 308/3; 326/3; 421/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 MFTINSIGRLGNQMGEXATLFALARMNGRLAFIPASMHNALAPIFR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.2%; Score 138.5; DB 2; Best Local Similarity 23.4%; Pred. No. 0.001; Matches 74; Conservative 48; Mismatches 105;
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A:Wolecule type: DNA
A;Residues: 1-955 <MIL
A:Cross-references: EMBL:281132; PIDN:CAB03434.1; GSPDB:GN00023; CESP:T26E4.4
A;Experimental source: clone T26E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 5
A;Introns: 50/1; 80/2; 140/3; 179/3; 218/2; 253/1; 278/1; 306/3; 325/1; 342/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T26E4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: T23309
R;McMurray, A.
Submitted to the EMBL Data Library, October 1996
A;Reference number: Z20013
                                                                                                                                                                                                       100 --LPVLHSDTAKKIPWQNYHLNDWMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKE 156
                                                                                                                                                                                                                                                        70 QHLPKLVRDALKYMGFDRVSQEIVFEYEPKLLKPSRLTYFYGYFQDPRYFDAISSLIKQT 129
                                                                                                                                                                                                                                                                                                               FTL-----HDHVREEAQAFLRGLR-VNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRG 210
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                                                            Gaps
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6.8%; Score 131; DB 2; Length 365;
Best Local Similarity 20.7%; Pred. No. 0.003;
Matches 61; Conservative 43; Mismatches 106; Indels
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                        22.9%;
                        Best Local Similarity 22.9
Matches 76; Conservative
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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FUT1_MOUSE
FUT1_RAT
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seq length: 2000000000
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Result

8

| Q61409 mus musculu |            |            |            | P87503 human adeno | P97846 rattus norv | P78357 homo sapien | P87379 xenopus lae | Q9z140 helicobacte | P23739 rattus norv | P47527 mycoplasma | 054991 mus musculu |
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| CN3B_MOUSE         | YFAS_ECOLI | GSPN VIBCH | GLO2_SYNY3 | DPOL_ADE04         | CTA1_RAT           | CTA1_HUMAN         | GRB2_XENLA         | RIBB_HELPJ         | SUIS_RAT           | Y285_MYCGE        | CTA1_MOUSE         |
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## ALIGNMENTS

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             Q10982: Q29044; O19100;
01-0CT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
(Fucosyltransferase 2).
                                                                                                                                                                                                                                                                                                                    MEDINE-97468270; PubMed=9321466; Masabanda J., Wigger G., Meigraink E., Fries R., Voegell P., Masabanda J., Wigger G., Stricker C., Neuenschwander S., Bertschinger H.U., Stranzinger G.; Two alpha(1,2) fucosyltransferase genes on porcine chromosome 6q11 are closely linked to the blood group inhibitor (S) and Escherichia are clisely linked (ECP187) loci."; Mamm. Genome 8:736-741(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thurin J., Blaszczyk-Thurin M.;

"Porcine submaxillary gland GDP-L-fucose: beta-D-galactoside
alpha-2-L-fucosyltransferase is likely a counterpart of the human
Secretor gene-encoded blood group transferase.";
J. Biol. Chem. 270:26577-26580(1995).
-! CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
-! PATHWAY: Glycosylation.
-! SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISIERNAE OF GOLGI (BY SIMILARITY).
                                                                                                                                                                                                               Eukaryota, Metázoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Cohney S., Mouhtouris E., McKenzie I.F.C., Sandrin M.S.;
Molecular cloning and characterization of the pig secretor type alpha(1,2)fucosyltransferase.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 69-334 FROM N.A. Petit J.M.; Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
340 AA
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PRT;
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MEDLINE=96064742; PubMed=7592879;
SIANDARD;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                               Sus scrofa (Pig).
                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
FUT2_PIG
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porphyromon

paracoccus

P05418 051825

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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:Deta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
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                                                                                                                                                                                                                                                                                                                                                                                    61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                             WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
-!- PATHWAY: Glycosylation.
-!- PATHWAY: Glycosylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos. NCHI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSTYVGYHYRRGDYVHVMPNVWKGYVADRRYLEQALDWFRARYRSPVFVVSSNGMAWCRE
                                                                                                                                                                                                                                                                                                                   STITHLOORIVKLOPLSEKELPMTTOMSSGNTESPEMRRDSEOHGNGELRGMFTINSIGR
                                                                                                                                                                                                                                                                                                                                           23 STIFHLOORMYKIQP--TWELOMVTQVT---TESP-----SSPQLKGMWTINAIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE
                                                                                                                                                LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

R -> H (IN REF. 3).
                                                                                                                                                                                                                                                                                         14;
                    EMBL; AF027304; AAC09170.1; -.
EMBL; X99621; CAA67932.1; -.
InterPro; IPR002516; GI_11.
Pfam; PF01531; GJycortransf_11; 1.
Transferase; GJycoryltransferase; GJycoprotein; Transmembrane; Golgi stack; Signal-anchor.
                                                                                                                                                                                                                                                         cch 75.5%; Score 1451; DB 1; Length 340; al Similarity 81.9%; Pred. No. 1.9e-115; 271; Conservative 26; Mismatches 20; Indels 14
                                                                                                                                                                                                                                  0629F1C04FC206AD CRC64;
                                                                                                         CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                  38987 MW;
           EMBL; U70881; AAB81883.1; -.
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185
251
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185
251
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340 AA;
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Q28113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Petit J.M.;
                                                                                                                                                                                                     CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                           CARBOHYD
CARBOHYD
                                                                                                                     RANSMEM
                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                            Query Match
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JW-2002 (Rel. 41, Last annotation update)
15-JW-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
(Fucosyltransferase 2) (Secretor blood group alpha-2-
fucosyltransferase) (Secretor factor) (Se) (SE2).
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SIGNAL-ANCHOR (IYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 STIFHLHORLEKMOPTWELEA-----LEPATMETPSRPOPRPOLKGMWTINAIGR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
LUMENAL, CATALIIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
W; F35AG33F1B7B9F68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE
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Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                         InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-95181460; PubMed-7876235;
Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.6%; Score 1414; DB 1; 78.9%; Pred. No. 2.5e-112;
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; Mismatches
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39320 MW;
                                                                                                                                                                                                                                                 EMBL; X99620; CAA67931.1; -.
                                                                                                                                                                                                                                                                                                                                                                     Golgi stack; Signal-anchor.
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344 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 261;
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ID DOT DOT SERVING CONTRACTOR CON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Extensive polymorphism of the FUT2 gene in an African (Xhosa)
population of South Africa.";
Hum. Genet. 103:204-210(1998)
-!- FUNCTION: CREATES A SOLUBLE PRECURSOR OLIGOSACCHARIDE FUC-ALPHA
(1,2)GALBEIA-) CALLED THE H ANTIGEN WHICH IS AN ESSENTIAL
SUBSTRATE FOR THE FIRAL STEP IN THE SOLUBLE A AND B ANTIGEN
SUBSTRATES BOT EXHIBIT DIFFERENT KW VALUES.
-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: GLYOSYLALIDE.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
-!- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY THE USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-!- ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-!- TISSUE SPECIFICITY: SMALL INTESTINE, COLON AND LONG.
-!- MISCELLANBOUS: THERE ARE TWO GENES (FUTI AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCCSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
     blood
                                                                                           [2]
SEQUENCE FROM N.A., AND VARIANT PHE-140.
MEDLINE=96199252; PubMed=8621666;
Kudo T., Iwasaki H., Nishihara S., Shinya N., Ando T., Narimatsu I.,
"Sequence and expression of a candidate for the human Secretor blood group alpha(1,2)fucosyltransferase gene (FUT2). Homozygosity for an enzyme-inactivating nonsense mutation commonly correlates with the
                                                                                                                                                                      system. II. Secretor gene inactivation by a novel single missense J. Biol. Chem. 271:9830-9837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              T., du Toit E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LONG ISOFORM.
GALACTOSIDE 2-L-FUCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GALACTOSIDE 2-L-FUCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
Signal-anchor; Golgi stack; Alternative initiation;
Blood group antigen; Polymorphism.
                                                                                                                                                                                                                                                                                                                         Koda Y., Soejima M., Wang B., Kimura H.;
"Structure and expression of the gene encoding secretor-type
galactoside 2-alpha-L-fucosyltransferase (FUT2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LUMENAL, CATALYTIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koda Y., Soejima M., Pang H., Schlaphoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOR SHORT ISOFORM.
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                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANT PHE-140.
                                                                                                                                                                                                                                                                                                                                                                                                       [4]
VARIANTS VAL-25, CYS-138 AND ASN-172.
MEDLINE=98431007; PubMed=9760207;
                                                                                                                                                                                                                                                                                                                                                                                   Eur. J. Biochem. 246:750-755(1997).
                                                           non-secretor phenotype.";
J. Biol. Chem. 270:4640-4649(1995).
                                                                                                                                                                                                                                                                                                             MEDLINE=97363210; PubMed=9219535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U17894; AAC24453.1; -. EMBL; D89327; BAA13944.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D87942; BAA21684.1; -. MIM; 182100; -.
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Kimura H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INIT_MET
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
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"Molecular cloning and expression of a GDP-L-fucôse:beta-D-galactoside 2-alpha-L-fucosyltransferase in murine gastrointestinal tract."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
6alactoside 2-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
(Fucosyltransferase 2) (FUT-III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHUND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 STIIHHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S.; "Molecular cloning and expression of a mouse GDP-L-Fucose: beta-D-adalactoside 2-alpha-L-Fucosyltransferase."; Submitted (DEC-1996) to the EMEL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 STIFHVOORLAKIOAM--WELPV-----OIPVLASTSKALGPSOLRGMWTINAIGR
                                                                                                                                                                                              I -> F (IN JAPANESE SEJ ALLELE; NON-
(GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                  73.3%; Score 1407.5; DB 1; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin B., Hayashi Y., Saito M., Sakakihara Y., Yanaqisawa M., Iwamori M.;
                                                                                                                                                                                                                                    /FTIG=VAR_003424.
D -> N (IN XHOSA POPULATION).
/FTIG=VAR_003425.
                                                                                   I -> V (IN XHOSA POPULATION).
/FIId=VAR_003422.
                                                                                                                                     R -> C (IN XHOSA POPULATION). /FIId=VAR_003423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                               12066D9CF175E13A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  1407.5,
No. 9e-112;
                                                              (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ICR; TISSUE=Gastrointestinal tract;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 PDSPFLKIFKPEAAFLPEWIGIAADLSPLLK 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
  N-LINKED (
N-LINKED (
N-LINKED (
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
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                                                                                                                                                                                                                                                                                                                                               39017 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            79.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
  188
282
308
25
                                                                                                                                           138
                                                                                                                                                                                                                                                                                    172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                            343 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                              138
                                                                                                                                                                                                 140
                                                                                                                                                                                                                                                                                    172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUT2 OR SEC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ICR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUT2_MOUSE
P97353;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
     CARBOHYD
                                CARBOHYD
                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                       VARIANT
                                                                                         VARIANT
                                                                                                                                              VARIANT
                                                                                                                                                                                                    VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                    FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
MISCELLANBOUS: THERE ARE TWO GENES (FUT1 AND SEC1) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLITRANSFERASE.
SIMILARITY: BELONGS TO THE GLYCOSYLITRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-tucosyltransferase 2 (EC 2.4.1.69) (Secretor blood group alpha-2-fucosyltransferase) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2) (Fucosyltransferase 2).
                                 PATHWAY: Glyoosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STITHLOORIVKLOPLSEKELPMTTOMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 PSTFVGVHVRRGDYVRVMFKVWRGVVADRGYLEKALDRFRARYSSPVFVVTSDDMAMCRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STIFHCHRL-----GIVPAPWASPSLVVFPPRHMPRE--GMFTIRVKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ
CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP alpha-L-fucosyl-1, 2-beta-D-galactosy.-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. ) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

40932853E37303B CRC64;
                                                                                                                                                                                                                                                                                                          EMBL; AF113532; AAD25551.1; -.
MGD; MGI.109374; Fut2.
InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 69.7%; Score 1338.5; DB 1 al Similarity 77.3%; Pred. No. 6.7e-106; 252; Conservative 21; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDSPFLKVFKPEAAFLPEWVGIPADL 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368
195
289
315
41464 MW;
                                                                                                                                                                                                                                                                                                                                                                                                        stack.
                                                                                                                                                                                                                                                                                               EMBL; Y09882; CAA71008.1;
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                                                                                                                                                                                                                                                                                                                                                                                                          Golgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42
195
289
315
368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      Signal-anchor;
DOMAIN
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Q10983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 252
                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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FUT2_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                              Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S.;
"Molecular cloning and expression of two types of rabbit betagalactoside alpha 1.2-fucosyltransferase.";
"J. Biol. Chem. 270:8844-88550(1995).
-!- FUNCTION: CREATES A SOLUBLE PRECURSOR OLIGOSACCHARIDE FUC-ALPHA ((1,2)SALBETR-) CALLED THE H ANTIGEN WHICH IS AN ESSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE SOLUBLE A AND B ANTIGEN SYNTHESIS PATHWAY. H AND SE ENZYMES FUCOSYLATE THE SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WHICH
                                                                                                                                                                                                                                                                                                                                    -1- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1, 2-beta-D-galactosyl-R.
-1- PATHWAY: Glycosylation.
-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STITHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 SIVFHCHQRLAL------VPAPWAYSARVVVVP------GHLPREGMWTINAMGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FURN IN INDIANA CLASARAND AS CACAL.
-1- TISSUE SPECIFICITY: SALIVARY AND LACTATING MAMMARY GLANDS.
-1- MISCELLANEOUS: THERE ARE THREE GENES (FUTI, FUT2 AND FUT3) WHI
ENCODE GALACTOSIDE 2-L-FUCCOSTITRANSFERASE IN RABBIT: THEY ARE
             Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi:
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LUMENAL, CÁTALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
1E2B831F9DA6CCB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002516; GT_11.
Pfam, PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXPRESSED IN A TISSUE-SPECIFIC MANNER.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .3e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.5%; Score 1296.5; 73.9%; Pred. No. 2.3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                            TISSUE=Brain;
MEDLINE=95238380; PubMed=7721792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40035 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X80225; CAA56512.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Golgi stack.
1 22
3 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44
197
291
317
354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                          SEQUENCE FROM N.A.
                                                                       NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
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STRAIN-BDIX
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Q10980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-b-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)F1 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFORMED AND EXPLANABLE PARTICLES.

1. CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1, 2-beta-D-galactosyl-R.

1. PATHWAY: Glycosyl-1, 2-beta-D-galactosyl-R.

1. SUBCELLUIAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.

1. TISSUB SPREDITION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.

1. TISSUB SPREDITION: AND LESSER EXTENT IN THYMUS, LUNG, STOMACH, SMALL INTESTINE, COLON, SPLEEN AND UPERUS. NOT EXPRESSED IN BRAIN. HEART, SKELETAL MUSCLE, KIDNEY, LIVER AND BONTE MARROW.

1. INSCELLANBOUS: THERE ARE TWO GENES (FUTI AND FUT2) WHICH ENCODE GALACTOSIDE 2-1-FUTOSIDE 2-1-FUTOSIDE STOMATHY 11
261 NIDASRGDVVFAGNGLEGSPAKDFALLTQCNHTVMT.GTFGFWAAYLTGGDTVYLANYTA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
1. 21F1D24CFE2C4106 CRC64;
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-NIH Swiss,

BEDIND-9745449; PubMed-9355741;

Domino S.E. Hiraiwa N., Lowe JB.;

Molecular cloning, Circmosomal assignment and tissue-specific expression of a murine alpha(1,2)fucosyltransferase expressed in thric and epidioymal epithelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
Signal-anchor; Golqi stack,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.5%; Score 1105.5; DB 1; Length 62.8%; Pred. No. 3.6e-86; ive 38; Mismatches 76; Indels
                                                                                                                                                             376 AA.
                                 301 PDSPFLKVFKPEAAFLPEWVGIPADLSPLL 330
                                                   321 PDSPFHLVFKPEAAFLPEWVGITANMGRAL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01531; Glyco_transf_11; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42255 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:109375; Fut1.
InterPro; IPR002516; GT_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Golgi stack
                                                                                                                                                           STANDARD:
                                                                                                                                                                                                                                                                             (Fucosyltransferase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
376
67
302
328
                                                                                                                                                                                                                                                                                                               musculus (Mouse)
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328
376 AA;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                     FUT1 MOUSE
009160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Simi
Matches 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (BC 2.4.1.69) (GDP-L-fucose:beta-begalactoside 2-alpha-L-fucosyltransferase 1)
75 ARMNGRLAFIPASMHNALAPIFRISLPVLESDTAKKIPWQNYHLNDWMEBRYRHIPGHFV 134
                          RFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPS-TFVGVHVRRGD 193
                                                                                                                                                                  253
                                                                                                                                                                                                         284
                                                                                                                                                                                                                                                313
                                                                                                                                                                                                                                                                                     344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN, MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
MISCELLANGOUS: THERE ARE TWO GENES (FWTI AND FOT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLATRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.
SIMILARIII: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                   194 YVEVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAG
                                                                                                                                                                               NGIEGSPAKDFALLTQCNFTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEA
                                                                                                                                                                                                                                                          Plau J.-P., Labarriere N., Dabouis G., Denis M.G.;
"Evidence for two distinct alpha(1,2)-fucosyltransferase genes
differentially expressed throughout the rat colon.";
Blochem. J. 300:623-626(1994).
-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom:
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Two distinct rat GDP-L-fucose:b-D-galactoside 2-alpha-L-fucosyltransferase genes.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            376 AA
                                                                                                                                                                                                                                                                                                               314 AFLPEWVGIPADLSPLLKALTPACPRSHFHL 344
                                                                                                                                                                                                                                                                                                                                                  345 AFLPEWVGINADLSPLQAQFDPWKPDSLFRL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soejima M., Wang B., Koda Y., Kimura H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94280382; PubMed=8010942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB015637; BAA31130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 169-310 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fucosyltransferase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Colon cancer;
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5

Gaps

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PLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFAL 74

Conservative

Similarity

Best Loca Matches

15 53

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01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 34, Last sequence update)
15-UDN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-Popalactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
FUTI OR RFT-I.
                                                                                                                                                                                                                                                                                                                                                                      135 RFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVN--GSQPSTFVGVHVRRG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 GNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPE 312
                                                                                      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                    53 PVAMYCLPYPSNASSGSPSCPE-----OSLLSGTWTITPGGRFGNOMGQYATLLAL 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE
                                                                                                                                                                                                                                                       PLSEKELPMTTQMSSGNTESPEMRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFAL
                                                                                                                                                                                                                                                                                                                                                                                                                             DYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                               ARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFV
                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: G1YCOSY1ation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI.
                                                                                                            UMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

C350C737C758B7F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                  11;
EMBL: L26009; AAB41514.1; -.
InterPro; IPR002516; GT_11.
Pfam: PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack.
DOMAIN 1 12 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                      DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S., Molecular cloning and expression of two types of rabbit betagalactoside alpha 1,2-fccsyltransferase.";
J. Biol. Chem. 270.8844-8850(1995)
--- CATALYIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = Galactosyl-R.
                                                                                                                                                                                                                                 77; Indels
                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                             Ouery Match
57.3%; Score 1101.5; DB 7
Best Local Similarity 62.3%; Pred. No. 7.8e-86;
Matches 207; Conservative 37; Mismatches 77,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 AA
                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAFLPEWVGIPADLSPLLKALTPACPRSHFHL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95238380; PubMed=7721792;
                                                                                                                                                                        42416 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIFICITY: BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                              376
64
302
328
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29
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328
376 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUT1_RABIT
Q10979;
                                                                                   TRANSMEM
                                                                                                                           CARBOHYD
                                                                                                                                         CARBOHYD
                                                                                                                                                        CARBOHYD
                                                                                                                                                                     SEQUENCE
                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
FUT1_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                  164
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (BC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1.2)FT 1)
(Fucosyltransferase 1) (Blood group H alpha 2-fucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 SEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 ------GIWTHPDGREGNOMGOYATLLALAQLNGRRAFILPAMHAALAPVFRITL 128
                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHVREEAQAFLRGLRV--NGSQPSIFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 STIIHLQQRIVK-----SGNIESPEMRRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O.F
                                                                                                                                                                                                                                                                                                               (CUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GICNAC. .) (POTENTIAL).

N-LINKED (GICNAC. .) (POTENTIAL).

N-LINKED (GICNAC. .) (POTENTIAL).

0A47A1786231525C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominigae; Homo.
GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUB-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS (MESODERMAL OR ENODDEMAL ORIGIN RESPECTIVELY.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                          Interpro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                              59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 1086; DB 1,
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                                                                                                                                                                                                                                                                                                                                                                                42098 MW;
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                                                                                                                                                                                                                                                        Golgi stack.
1 12
3 29
                                                                                                                                                                                               EMBL; X80226; CAA56513.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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66
301
327
373 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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SEQUENCE FROM N.A.
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DOMAIN
1
TRANSMEM 13
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                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Sim
Aatches 206;
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                                                                                                                                                                                                                                                                                                                                  CARBOHYD
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FUT1_HUMAN
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[3]
SEQUENCE FROM N.A.
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R InterPro; IPR002516; GT_11.

R Ffam; PF01531; Glyco_transf_11; 1.

Pfam; PF01531; Glyco_transf_11; 1.

Pfam: PF01531; Glyco_transf_11; 1.

R Transmembrane;

KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;

KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;

KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;

FT TRANSMEM 9 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

FT CARBOHYD 126 365 LUMENDLY (POTENTIAL).

FT CARBOHYD 65 65 N-LINKED (GLCNAC. ..) (POTENTIAL).

FT CARBOHYD 327 327 N-LINKED (GLCNAC. ..) (POTENTIAL).

FT VARIANT 154 154 Y -> C (IN BOMBAY H-).

AFTIG=VAR_003417.

AFTIG=VAR_003417.

AFTIG=VAR_003417.

AFTIG=VAR_003417.

AFTIG=VAR_003417.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI.
POLYMORPHISM: NONFUNCTIONAL MOTANY OF FUTI ARE THE CAUSE OF THE H-
BOMBAY BLOOD GROUP.
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97445117; Pubmed-9299444;

Koda Y., Soejima M., Johnson P.H., Smart E., Kimura H.;

Koda Y., Soejima M., Johnson P.H., Smart E., Kimura H.;

Koda Y., Soejima M., Johnson P.H., Smart E., Kimura H.;

Indian Bombay phenotype at ABO blood group system.;

Blochem. Biophys. Res. Commun. 238:21-25(1997).

-! FUNCTION: CREATES A SOLUBLE PRECURSOR OLIGOSACCHARIDE FUC-ALPHA SURSTRATE FOR THE FINAL STEP IN THE SOLUBLE A AND B ANNIGAL SUBSTRATE FOR THE FINAL STEP IN THE SOLUBLE A AND B ANNIGAL SYNTHESIS BATHARY. H AND SE BRZYMES FUCCOSYLATE THE SAME ACCEPTOR SYNTHESIS BUT EXHIBIT DIFFERENT KM VALUES.

-! CAPALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + Albhar-L-fucosyl-R.
              Larsen R.D., Ernst L.K., Nair R.P., Lowe J.B.;
"Modecular cloning, sequence, and expression of a human GDP-L-
"Modecular cloning, sequence, and expression of a human GDP-L-
fluose:beta-D-galactoside 2-alpha-L-fucosyltransferase cDNA that can
form the H blood group antigen.";
Proc. Natl. Acad. Sci. U.S.A. 87:5674-6678(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANDOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERMAL OR ENCODERMAL ORIGIN RESPECTIVELY.

SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                   VARIANT HIS-164.
MEDLINE-94286534; PubMed=7912436;
Kelly R.J., Ernst L.K., Larsen R.D., Bryant J.G., Robinson J.S.,
                                                                                                                                                                                                                                                                                                    "Molecular basis for H blood group deficiency in Bombay (Oh) and
                                                                                                                                                                              of
                                                                                                                                                  Wagner F.F., Flegel W.A.; Polymorphism of the hallele and the population frequency sporadic nonfunctional alleles."; Transfusion 37:284-220(1997).
                                                                                                                                                                                                                                                                                                                    para-Bombay individuals.";
Proc. Natl. Acad. Sci. U.S.A. 91:5843-5847(1994).
                                                                                                                SEQUENCE FROM N.A., AND VARIANT ALLELES. MEDLINE=97240210; Pubmed=9122901;
MEDLINE=90370848; Pubmed=2118655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M35531; AAA52639.1; -. EMBL; Z69587; CAA93435.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:4012; FUT1.
MIM; 211100; -
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                                                                                                                                                                                                                                                                                                                                                                       VARIANT ARG-242
                                                                                                                                                                                                                                                                                          Lowe J.B.;
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FUT1_PIG STANDARD: PRT; 365 AA. 029043; 019101; 01.00V-1997 (Rel. 35, Created) 01.00V-1997 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 NALAPIERISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 RPEILKEFTLHDHVRREBAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89
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Meljerink E., Fries R., Voegeli P., Masabanda J., Wigger G., Stricker C., Neuenschwander S., Bertschinger H.U., Stranzinger G.; "Two alpha(1,2) fuccsyltransferase genes on porcine chromosome 6q11 are closely linked to the blood group inhibitor (S) and Escherichia Manmm. Genome 8:736-741(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.7%; Score 1051.5; DB 1; Length 365; 63.3%; Pred. No. 1.3e-81; live 37; Mismatches 73; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VAR_003421.
4F4442EC375C9D9E CRC64;
/FTIG=VAR_003418.
L -> R (IN BOWBAX H-).
/FTIG=VAR_009709.
V -> E (IN BOWBAY H-).
/FTIG=VAR_004419.
A -> V (IN BOWBAY H-).
/FTIG=VAR_003420.
M -> C (IN BOWBAY H-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                41251 MW;
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                                                                                                                                                       259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 195; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fucosyltransferase
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                                                    242
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                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

LUMBEND, CATALITIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 PVAIFCLAGTPVHPNASDSCPKH-PASLSGTWTIYPDGRFGNOMGOYATLLALAQLNGRQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 AFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 SWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meijerink E., Neuenschwander S., Fries R., Dinter A.,
Bertschinger H.U., Stranzinger G., Voegeli P.;
"Expression and activity of porcine alpha(1,2)fucosyltransferases
"Expression and activity of porcine alpha(1,2)fucosyltransferases
Getermine erythrocyte antigen precursor o status and susceptibility
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-- CATALYITA CATIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
--- PATHWAY: Glycosylation.
--- SUBCELULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAR OF GOLGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                  -!- MISCELLANEOUS: THERE ARE TWO GENES (3UT1 AND FUT2) WHICH ENGALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U70883; AAB81884.1; --
EMBL; AF136969; AAF59833.1; --
InterPro; IPR005516; C__l1; C__l1;
Pfam; PF01531; Glyco_transf__l1; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
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                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
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DAFCE77E89A29D75 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L50534; AAB02984.1; -.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
63-JUN-2002 (Rel. 41, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LINKED (GLCNAC. . .) (POTENTIAL).
14DECEB7C2E6384A CRC64;
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"Evidence for two distinct alpha(1,2)-fucosyltransferase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·;
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Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
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Pred. No. 1.1e-64;
0; Mismatches 1; Indels
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                   AA.
             159
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STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
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RESULT 12

RESULT 11

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                                                                                                                                                                                   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Carton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Morrimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                          01-FEB-1994 (Rel. 28, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Puttive glycosyl transferase C06El.7 in chromosome III (EC 2.-.-).
C06El.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 SIGRLGNQMGEYATLFALARMNGR--LAFIPASMHNALAPIFRISLPVLHSD------ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRGYLEKALDMFRAR------YSSPVFVVTSNGMAWCRENINASRGD 248
                                                                                                  Eukaryota; Metazoa; Nematoda: Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --TAKKIP------WQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 TLHDHVREEAQAFIRGL----RVNGSQPSTFVG---VHVRRGDYV---HVMPNVWKGVVA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SFIKPALEFIKEREQKDVNKKMLTVIMGDDPDFEAKMF----EGTVRAKKEAKIEETT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 VVFAGNGIEGSPAKDFALL-TQCNHTIMTI--GTFGIWAAYLAGGDTIYLANY-TLPDSP 304
                                                                                                                                                                                                                                                                                                                                  ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 HNKATKVPLSEKCCIFDNPDKFNNISSEYLHLTGHFYQ-----SWKYF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88;
                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.7%; Score 168; DB 1; Length 365; 22.0%; Pred. No. 7.2e-07; tive 48; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPRO0516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Hypothetical protein; Transferase; Glycosyltransferase.
SEQUENCE 365 AA; 41991 MW; B5FBCA363F31977F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
-
        365 AA.
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                                                                                                               Rhabditidae, Peloderinae; Caenorhabditis
NCBI_TaxID=6239;
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                                                                                                                                                            STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L16559; AAA27932.2; -.
WormPep; C06E1.7; CE30483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71; Conservative
      STANDARD;
                                                                                                                                                                                                                                                                                                                                                 Nature 368:32-38(1994).
                                                                                       Caenorhabditis elegans.
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        Waterston R.;
   CAEEL
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REVISIONS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flowers C.C., Eastman E.M., O'Callaghan D.J.; "Sequence analysis of a glycoprotein D gene homolog within the unique short segment of the EHV-1 genome."; Virology 180:175-184(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSIGRLGNQMGEYAT--LFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPW 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 LYRRVIEIDGRRIYTDFSVTIPSERCPIAFELNFGN---PDRCKMPBQYSRGE---VFTR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92263758; pubMed=1316673; Colle C.F. III, Flowers C.C., O'Callaghan D.J.; Open reading frames encoding a protein. Winase, homolog of 91ycoprotein gX of pseudorabies virus, and a novel glycoprotein map within the unique short segment of equine herpesvirus type 1."; Virology 188:545-557(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GCONAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYCOPROTEIN D. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Equine herpesvirus type 1 (strain Kentucky A) (EHV-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323CDCA9C9762F05 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                         update)
on update)
                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein D precursor (Glycoprotein 17/18) GD OR GP17/18 OR 72.
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                                                                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=91082407; PubMed=1845821;
305 FLK-VFKPEAAFLPEWVGIPAD 325
                                                          335 YKKGVLDPDDFFVPSWTSIMLD 356
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                                    114 ONYHLNDWMEERYRH----IPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQ 168
                                                                       332 DNHPGFDSVESEITQNKTDPKPGQADPKPNQPFKWPSIKHLVPRL------DEVDEVIE 384
           --FARPVPP 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAJOR FIMBRIAL SUBUNIT PROTEIN, TYPE III. 7FBE4FBF427EA2AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fujiwara T., Morishima S., Takahashi I., Hamada S., "Molecular cloning and sequencing of the fimbrilin gene of Porphyromonas gingivalis strains and characterization of recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Finbrillin is the structural subunit of the fimbriae, that are filamentous appendages on the cell surface. Fimbriae of P.gingivalis are recognized as a major virulence factor as they mediate cell adhesion and play an important role in invasion of
                                                                                                           169 AFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSP 226
                                                                                                                                    385 PVTKPPKTSKSN-STFVGISVGLGIAGLVLVGVILYVCLRR---KKELKVCTERLDSP 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional differences among FimA variants of Porphyromonas gingivalis and their effects on adhesion to and invasion of human epithelial cells.":
Infect. Immun. 70:277-285(2002).
                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Major fimbrial subunit protein, type III precursor (Fimbrillin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Fimbria.
SIMILARITY: BELONGS TO THE P.GINGIVALIS FIMBRILLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21614934; PubMed=11748193;
Nakagawa I., Amano A., Kuboniwa M., Nakamura T., Kawabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 89; DB 1; Length 353
; Pred. No. 3.3;
38; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides; Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 197:241-247(1993).
288 RFLGEFNFPQGEHMTWVKFWFVYDGGNL---PVQFYEAQA--
                                                                                                                                                                                                                                                  353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION, AND CLASSIFICATION INTO TYPES.
                                                                                                                                                                                                                                                                                                                                                                                                                             Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94071950; PubMed=7902712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 MP
38024 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D17801; BAA04627.1;
                                                                                                                                                                                                                                            STANDARD;
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353 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                    (Fimbrilin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=6/26
                                                                                                                                                                                                                                        FMA3_PORGI
Q51826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hamada S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                     191 ITFNGAYSPANYTHVDWLGRDYTEIGAATVNTPKGF----YVLESTYAQNAGLRPTILC 245
                                                                                                                                              155 --KEFTLHDHV----REEAQAFLRGLRVNGSQPSTF--VGVHVRRGDXVHYMPNVWKGVV 206
                                                                                                                                                                                   246 VKGKLTKHDGTALSSEEMTAAFNAGWIVANNDPTTYYPVLVNFESNNYTYTGEAVEKGKI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 19-208.
MEDLINE-20139694; PubMed=10673428;
Hallberg B.M., Bergfors T., Boeckbro K., Pettersson G., Henriksson G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A new scaffold for binding haem in the cytochrome domain of the extracellular flavocytochrome cellobiose dehydrogenase.";
Structure 8:79-88(2000).
-!-FUNCTION: DEGRADES BOTH LIGNIN AND CELLULOSE. OXIDIZES CELLOBIOSE
-!-CAPALYTIC ACTIVITY: Cellobiose + a quinone = cellobiono-1,5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li B., Nagalia S.R., Renganathan V.;
"Cellobiose dehydrogenase from Phanerochaete chrysosporium is encoded
                                                                          ----IPWQNYHLNDWMEERYRHI-----PGHFVRFTGYPCSWTFYHH--LRPEIL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Basidiomycota; Hymenomycetes; Homobasidiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cellobiose dehydrogenase precursor (EC 1.1.5.1) (CDH) (Cellobiose-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lactone + a phenol.
--- COFACTOR: ONE FAD AND ONE HEME B.
--- SUBCELLULAR LOCATION: Secreted.
--- SIMILARITY: IN THE C.TERMINAL SECTION; BELONGS TO THE GMC
                                                                                                                                                                                                                         207 ADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGI 256
                                                                                                                                                                                                                                                306 VRNHKFDINLTITGPGTNNPENPIT-----ESANLNVNCVVAAWKGV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li B., Nagalla S.R., Renganathan V.; "Cloning of a cDNA encoding cellobiose dehydrogenase, hemoflavoenzyme from Phanerochaete chrysosporium."; Appl. Environ. Microbiol. 62:1329-1335(1996).
74 LARMNGRLAF--IPASMHNALAPIFRISLPVLHSDTAKK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Basidiomycota; Hymenomycete
Aphyllophorales; Corticiaceae; Phanerochaete.
NCBI_TaxID=5306;
                                                                                                                                                                                                                                                                                                                                                              773 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by two allelic variants.";
APpl. Environ. Microbiol. 63:796-799(1997).
                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=0GC101;
MEDLINE=97077226; PubMed=8919793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=0GC101;
MEDLINE=97176414; PubMed=9023960;
                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phanerochaete chrysosporium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U46081; AAC49277.1; -.
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                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quinone oxidoreductase).
CDH-1 AND CDH-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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78;

80 LITELTEGNQEAAGLIMTAEPVEVTLVAGN------NYYGYDGSQGGNQISQGTPLE 130

23 MIIQMSSGNTESPEMRRDSEQ-----HGNGELRGMFTINSIGRLGNQMG---EYATLFA 73

64; Conservative

Matches

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CELLOBIOSE DEHYDROGENASE.
HEME DOMAIN.
OXIDOREDUCTASE.
HEME LIGAND.
HEME LIGAND.
HEME LIGAND.
HEME (ADP PART) (POTENTIAL).
W; 54F721E779AA4D7B CRC64;
EMBL; U50409; AAB92262.1; -.
DR
DR
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11; 131 GHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRG------LRVNGSQPS 182 337 GDFSSSVGWPSSWTNHAPYTSKLSSRLPSTDHPSTDGQRYLEQSFNVVSQLLKGQGYNQA 396 54; Gaps Query Match
4.6%; Score 89; D3 1; Length 773;
Best Local Similarity 22.0%; Pred. No. 8.6;
Matches 49; Conservative 29; Mismatches 91; Indels qq δ

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Search completed: May 27, 2003, 15:07:13 Job time: 11.478 secs

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09jk44 rattus norv 055025 rattus norv 035087 rattus norv 095127 mus musculu 070504 mus musculu 0920w2 mus musculu 0920w3 mus musculu 074486 gorilla gor 077486 gorilla gor 077487 gorilla gor 09tud5 gorilla gor 09tud5 pan troglod 029505 oryctolagus 077487 pongo pygma 09ttc7 hylobates 1
                                                            May 27, 2003, 15:01:52 ; Search time 40.5157 Seconds (without alignments) 1932.533 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                             1 MASAQVPFSFPLAHFLIFVF......RSHFHLKAKGVTCYVAGRAF 380
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                   671580 seqs, 206047115 residues
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Listing first 45 summaries
                                          OM protein - protein search, using sw model
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| 7712 cercopit<br>9450 homo sap<br>920t3 mus mus<br>4338 homo sap<br>920t2 mus spi | 920t4 mus muscu<br>91773 mus muscu<br>9wue6 rattus no<br>ts15 macaca fas<br>ttc9 eulemur fu<br>tudl macaca mul<br>tudl macaca mul | 94ty3 bos tau<br>09f128 mus mu<br>095327 mus mu<br>0920w5 mus mu<br>0920w4 mus sp<br>04ty7 bos tau<br>9tud4 gorilla | tueb eulemur xxb6 homo sap x05 homo sap 267 macaca m 267 macaca f 267 mocaca f 267 homo sap 506 homo sap |
|---|---|---|--|
| 3 6 077712<br>2 4 099450<br>8 11 0920T<br>6 4 014338<br>8 11 0920T                | 11 091014<br>0 11 091013<br>11 091013<br>12 09115<br>13 6 091101<br>16 09101<br>16 09101  | 68 6 099TY3<br>77 11 094L28<br>77 11 095327<br>77 11 0920W4<br>66 6 09TY7<br>66 6 09TUBF                            | 04040044   |
| 2. 17. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2.                                     | 363.5<br>363.5<br>363.5<br>1343 66.1<br>1319 64.9<br>266.5<br>62.3<br>24.5<br>61.2<br>3   |   | 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5  |
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## ALIGNMENTS

| DESULT 1  10 09JK44 PRELIMINARY; PRT; 380 AA.  10 09JK44 PRELIMINARY; PRT; 380 AA.  10 09JK44 PRELIMINARY; PRT; 380 AA.  10 01-0CT-2000 (TrEMBLTE1. 15, Last sequence update)  10 1-0CT-2000 (TrEMBLTE1. 15, Last sequence update)  10 1-MAR-2002 (TrEMBLTE1. 15, Last sequence update)  11 01 01 04   |                       | , o + a               | Jace)<br>Jpdate) | Craniata; Vertebrata; Euteleostomi;<br>Sciurognathi: Muridae: Murinae: Rattus |                  | H<br>E                                |   | equired tor optimum enzyme            | J databases.                            |  | )5C CRC64;   | 3 11; Length 380; 0; Indels 0; Saps 0; | KELPMITQMSSGNIESPEMR 60 |  | IGRLAFIPASMHNALAPIFRI 120 | [ | 007 8000 11000 11000 10000                                       |
|--|-----------------------|-----------------------|------------------|---|------------------|---------------------------------------|---|---------------------------------------|---|--|--|--|-------------------------|--|---------------------------|---|--|
| ರಿಗಳ ಕ್ಷಮಿಗಳು ಕ್ಷಮಿಗಳ | PRELIMINARY; PRT; 380 | (TrEMBLrel, 15, Creat |                  |   | QUENCE FROM N.A. | erwood A.L., Stroud M.R., Levery S.B. | n amino acid region at the N-terminus o | tivity and interaction with lipids."; | omitted (MAY-2000) to the EMBL/GenBank/ |  | ycosyltransferase; Transferase.<br>QUENCE 380 AA; 42742 MW; 920692C966 | 100.0%;<br>100.0%;<br>ztive 0;         |                         | 1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQ |                           |   | 21 SLPVLHSDTAKKIPWONYHLNDWMEERYRH;PGHFVRFTGYPCSWTFYHH;RPF11,8FFT |

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                                                                                                                                                                                                                                                                                                                                  MEDILINE-98342056; PubMed=9675030; Sherwood A.L., Holmes B.H.; "Cloning and expression of the catalytic domain from rat hepatoma H35 cell GDP-fucose: GMI alpha 1->2fucosyltransferase, an enzyme which is activated during early stages of chemical carcinogenesis in rat
240
                                               240
                                                                 241 FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
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                                                                                                       TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACP 360
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                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha 1,2 fucosyltransferase (Fragment).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLFVLHSDTAKKIPWQNYHLNDWMEER 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 AA; 39738 MW; 609D64EB222C9585 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1896; DB 11;
Pred. No. 3.8e-164;
0; Mismatches 0;
                                                                                                                                                                                                             353 AA
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EMBL; AF042743; AAC14695.1; -.
InterPro; IPR002516; GT_11,
FEMP: PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
NON_TER
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100.0%; Pre
0; '
                                                                                                                                                       RSHFHLKAKGVTCYVAGRAF
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                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                             STRAIN-BUFFALO RAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353;
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Best Local 8
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Matches
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SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata, Craniata; Vertebrața; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxiD=10116;
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
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LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF
                       TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fucosyltransferase genes.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB006138; BAGA1742.1;
Interpro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltranfarase; Transferase.
SEQUENCE 3554 AA; 39995 MW; 8636444888215BA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soejima M., Wang B., Koda Y., Kimura H.; "Two distinct rat GDP-L-fucose:b-D-galactoside 2-a-L-
                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 5.8e-163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                      (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=COLON CANCER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Q9R275;
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Pfam; PF01531; Glyco_transf 11; 1.
Glycosyltransferase; Transferase.
SEQUENCE 347 AA; 39215 MW; 616C
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                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                            Best Local Similarity
Matches 317; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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"Molecular Cloning, Genomic Mapping, and Expression of Two Secretor Blood Group alpha (1,2)Pucosyltransferase Genes Differentially Genomic Mapping, and Expression of Two Secretor Blood Group alpha (1,2)Pucosyltransferase Genes Differentially J. Biol. Chem. 276:23748-23756(2001).

BMOL. Chem. 276:23748-23756(2001).

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                                                                                                               Bureau V., Marionneau S., Cailleau-Thomas A., Le Moullac-Vaidye B.,
Liehr T., Le Pendu J.;
"Comparison of the three rat GDP-L-fucose: beta-D-galactoside 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                               InterPro; IPR002516; GT_11.
Pfam: PF01531; G1yco_transf_11; 1.
G1ycosyltransferase: Transferase.
SEQUENCE 354 AA; 39983 MW; 123E8C8379E8559E CRC64;
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01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha(1,2)fucosyltransferase FUT2 (EC 2.4.1.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1878; DB 11;
Pred. No. 1.7e-162;
                                                                                                                                                                                                         alpha-L-fucosyltransferases FTA, FTB and FTC.";
Eur. J. Biochem. 268:1006-1019(2001).
EMBL; AF131238; AAD24469.1; -.
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MEDLINE=21316545; PubMed=11323419;
                                                         STRAIN=BDIX;
MEDLINE=21099374; PubMed=11179967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.4%;
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                                                                                                                   1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
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                                                                                                                                                     18: LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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      Length 347;
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01-AUG-1998 (TIEMBLIEL. 07, Last sequence update)
01-AMR-2002 (TIEMBLIEL. 20, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 TFGIWAAYLAGGDTIYLANYTLPDSPFLKIFKPAAAFLPEWMGIPADLSPLLK
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                                                                 Indels
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   DB 11;
82.4%; Score 1674.5; DB 1389.8%; Pred. No. 5.3e-144;
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                                                           12; Mismatches
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EMBL; AF064792; AAC16887.1; -.
MGD; MGI:109374; Fut2.
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01-DEC-2001 (
01-DEC-2001 (
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SEQUENCE
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                                                       RESULT 8
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"Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AB039123; BAB68647.1;
-InterPro; IPR002516; GT_11.
Glycosyltransferase; Transfell; 1.
Glycosyltransferase; Transferase.
NON_TER 321
SEQUENCE 321 AA, 36560 MW, 5B7D19BA6D4B5394 CRC64;
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                                                                                                                 FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
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                          LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                 234 FRARYSSPVFVVTSNGMAWCRENINTSLGDVVFAGNGIEGSPAKDFALLIQCNHTIMTIG
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                               353
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
FUT2.
                                                                                                                                                                                                                                                                      TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
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321 AA; 36560 MW; 5B7D19BA6D4B5394 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 FTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 NGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74
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STRAIN=VARIOUS STRAINS;
Liu Y., Kiteno T., Koide T., Shiroishi T., Moriwaki K., Saitou N.;
"Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 FLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murisae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 321;
                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Five Mus musculus subspecies ", Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. BMBL, AB039115; BAB68638.1; --
EMBL, AB039115; BAB68640.1; --
EMBL, AB039116; BAB68641.1; --
EMBL, AB039119; BAB68642.1; --
EMBL, AB039119; BAB68643.1; --
EMBL, AB039120; BAB68643.1; --
EMBL, AB039120; BAB68644.1; --
EMBL, AB039120; BAB68644.1; --
EMBL, AB039120; BAB68645.1; --
EMBL, AB039120; BAB68645.1; --
EMBL, AB039120; BAB68645.1; --
EMBL, AB039120; BAB68645.1; --
EMBL, AB039120; BAB68644.1; --
EMBL, AB039120; BAB68645.1; --
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36516 MW; 0622D3BB503B72D1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.2%; Score 1547.5; DB 1.89.0%; Pred. No. 1.7e-132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Mismatches
321
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(TrEMBLrel. 19, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002516; GT_11.
Pfam: PF01531; Glyco_transf_11; 1
Glycosyltransferase; Transferase.
                                                                                                                                                      (EC 2.4.1.69) (Fragment).
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                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 AA;
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Best Local Similarity
Matches 292; Conserv
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Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.; "The old crigin of a null allale se428 of the human ABO-secretor type alpha(1,2) fuccosyltransferase gene (FUT2),"; submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                            121 SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meduly R.J., Ronquier S., Giorgi D., Lennon G.G., Lowe J.B.;
"Sequence and expression of a candidate for the human secretor blood group alpha(1.7) fucosyltansferase gene (FUT2).";

EMBL; AB015635; BAA31128.1; -...
InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transf_11; 1.
Glycosyltransferase: Transf_11; 1.
SEQUENCE 343 AA; 38973 MW; 894E28BD74AEBFBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;
"Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucosyltansferase gene (FUT2).";
J. Biol. Chem. 270:4640-4649(1995).
EMBL; AB015634; BAA31127.1;
InterPro: IPR002515; Gr_11.
Glycosyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                   1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                                                                           241 FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 FRARYSSPIFVVTSNGMAMCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 TFGIWAAXLTGGDTIXLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLK 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.6%; Score 1495.5; DB 6; Length 343;
                                                                                                                                                                                                                                   DB 6; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 TRGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes (Chimpanzee).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38999 MW; B849D7E152852081 CRC64;
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20, Last annotation update)
                                                                                                                                                                                                             AA.
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MEDLINE=95181460; FubMed=7876235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha(1,2)fucosyltransferase
                                                                                                                                                                                                                                                                          Matches 277; Conservative
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                                                                                                                                                                                                                              Query Match
Best Local Similarity
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01-MAR-2002
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                                                                                                                                                                                                        STRAIN=NJL/MSF;
Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.;
"Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE FROM N.A. SOEjima M., Takenaka O., Kimura H.; Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.; The old origin of a null allele se428 of the human ABO-secretor type alpha(1,2) fucosyitransferase gene (FUT2)."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTINSIGRIGNQMGEYATLFALARMNGRLAFTPASMHNALAPIFRISLPVLHSDTAKKIP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 FTINSIGRLGNQMGEYATLFALARMNGRLAFIPESMHNALAPIFRISLPVLHSDIARRIP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FLIFVFVTSTIIHLQQQIVKLQTLSEKEL-QAVQMSSPNAARTDMQQ-----SAKLQGI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 FLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTS
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                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
NCBI_TaxID=9593,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.4%; Score 1532.5; DB 11; Length 321; llarity 88.4%; Pred, No. 4e-131; Conservative 13; Mismatches 18; Indels 7;
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
2.4.1.69) (Fragment).
                                                                                                                                                                                                                                                                     Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AB039122; BAB68646.1;
InterPro; IRR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        321 321
321 AA; 36464 MW; FF5304CD150F774A CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
Alpha(1,2) fucosyltransferase.
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                                                                                  musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Local s.
290;
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SEQUENCE
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Matches

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181 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Mismatches
                                                                                                                                                                                           338
                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                               MOI. Biol. Evol. 17:337-351(2000).
EMBL; AF080604; AAF14066.1; -.
InterPro; IPR602516; GT_11.
Pfam: PF01531; Glyco_transf_11; 1.
                                                                                                                                                                                                                       01-MAY-2000 (TEMBLEEL 13, Last
01-MAR-2002 (TEMBLEEL 20, Last
Alpha (1,2) fucosyl transferase.
FUT2.
                                                                                                                                                                                                                                                                           Pan troglodytes (Chimpanzee)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 274; Conservative
                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                           Q9TUD5
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Q9TUD5
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                                                                                                       241 FRARYSSPYFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLIQCNHTIMTIG 300
                                                                                                                                        SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
                                                                                                                                                     110 TLPVLHSATASRIPWQNYHLNDWMEEEYRHIPGEYVRFTGYPCSWIFYHHLRQEILQEFT 169
                                                                                                                                                                                       LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM 240
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                       Gaps
                                                                                         61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
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                                                                   1 MLVVQMPFSFPVAHFILFVFTVSTIFHVQQRLAKIQAM--WELPV------QIPVLA 49
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                                            1 MASAQVPFSFPLAHFLIFVFVTSTITHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR
                                                                                                                                                                                                                                                   Gorilla gorilla (gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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                                                                                                                                                                                                                                                                                               301 TFGIWAAYLAGGDIIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apoil P.-A., Roubinet F., Despiau S., Mollicone R., Oriol R., Blancher A.;
                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
No. 1e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.6%; Score 1495.5; DB 78.2%; Pred. No. 1e-127;
      78.2%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                      343 AA
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EMBL: AF080606; AAF14068.1; '.
Interpro; IPR002516; GT_11.
Pfam: PF01531; Glyco_transf_11; 1.
Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha (1,2) fucosyl transferase.
                     276; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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         Best Local Similarity
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SEQUENCE FROM N.A.
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                   Matches
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Q9TUD3
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Apoil P.-A., Roubinet F., Desplau S., Mollicone R., Oriol R.,
Blancher A.;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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Hitcshi S., Kojima N., Kanacawa I., Tsuji S.;

"Molecular cloning and expression of a third type of rabbit GDF-L-
fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase.";

J. Biol. Chem. 27:116975-16981(1996)

-!- FUNCTION: CREATES A MEMBRANE-ASSOCIATED PRECURSOR OLIGOSACCHARIDE
FUC-ALPHA((1,2)GALBETA-) CALLED THE HANTIGEN WHICH IS AN
ESSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE MEMBRANE-ASSOCIATED
A AND B ANTIGEN SYNTHESIS PATHMAY. HAND SE ENZYMES FUCOSYLATE THE
SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.

-!- CATALYMIC ACTIVITY: GDF-L-FUCOSE + BETA-D-GALACTOSYL-R = GDF +
ALPHA-L-FUCOSYL-1, 2-BETA-D-GALACTOSYL-R = GDF +
                                                       01-FEE-1997 (TrEMBLrel. 02, Created)
01-FEE-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Galactoside 2-L-fucosyltransferase 3 (EC 2.4.1.69) (Secretor blood group ALPHA--tucosyltransferase) (GDP-L-fucose:beta-D-galactoside 2-ALPHA-L-fucosyltransferase) (ALPHA(1,2)FT) (Fucosyltransferase 3);
Oryctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERRARE OF GOLGI.
-i- TISSUE SPECIFICITY: ADULT GASTROINESTINAL TRACT AND COLON.
-i- MISCELLANEOUS: THERE ARE THREE GENES (FUT1, FUT2 AND FUT3) WHICH
ENCODE GALACTOGIDE 2-L-FUCOSYLTRANSFERASE IN RABBIT. THEY ARE
EXPRESSED IN A TISSUE-SPECIFIC MANNER.
-i- SIMILARITY: STRUCTURAL SIMILARITY WITH THE OTHER MAMMALIAN
GLYCOSYLTRANSFERASES.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MÁSAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 PTSQRAPSRPLGGMWTINAMGRLGNQMGEYATLYALAKENGRPAYIPAQMHSTLAPIFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

746F7007309862A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X91269; CAA62669.1; -
Interpo; IPR002516; GT_11.
Pfan; PF01531; GTyCo transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.5e-127;
347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.3%; Score 1488.5; 78.2%; Pred. No. 4.5e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
   PRT;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-GASTROINTESTINAL TRACT;
MEDLINE-96279281; PubMed-8663168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 N
39469 MW;
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   PRELIMINARY;
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192
286
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192 1
286 2
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                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276;
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CARBOHYD
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SEQUENCE
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TRANSMEM
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029505
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SEQUENCE FROM N.A. Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.; Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.; "The old origin of a null allele se428 of the human ABO-secretor type alpha(1,2), fucosyltransferase gene (FUT2)."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 STSKALGPSQLRGIWIINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.; "Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucosyltansferase gene (FUT2).";
J. Biol. Chem. 270:4640-4469(1995).

EMBL; AB015636; BAA31129-1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 FRARYSSPIFVVTSNGMAWCQENIDISHSDVVFAGDGIEGSPAKDFALLTQCNHIMTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEWR
                  294 TFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWVGINADLSPLLK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.2%; Score 1487.5; DB 6; Lengum
77.9%; Pred. No. 5.4e-127;
... ...matches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002516; GT_11.
Pfan: PF01531; Glyco_transf_11; 1.
Glycosyltransferase: Transferase: SEQUENCE 343 AA; 38973 WW; 2BD4D2A9704£4A0C CRC64;
                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95181460; PubMed=7876235;
                                                                                                                                                                                                               Alpha(1,2) fucosyltransferase.
                                                                                                                                                                                                                                                    Pongo pygmaeus (Orangutan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 77.9 Matches 275; Conservative
                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9600;
                                                                                                                                                            01-NOV-1998
01-NOV-1998
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09jk44 rattus norv 055025 rattus norv 035087 rattus norv 09r275 rattus norv 09j127 mus musculu 070504 mus musculu 0920w3 mus musculu 0920w3 mus musculu 07746 gorilla gor 09tud3 pan troglod 077485 pan troglod 077487 pongo pygma 099450 homo sapien
                                                                                                                                                        May 27, 2003, 15:01:52 ; Search time 38.17 Seconds (without alignments) 1932.533 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                 1921
1 STIIHLQQRIVKLQPLSEKE......RSHFHLKAKGVTCYVAGRAF 358
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  671580 seqs, 206047115 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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    protein search, using sw model

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Q9SK275
Q9R275
Q9JL27
Q920W3
Q91VF0
Q920W3
Q7TUD5
Q9TUD5
Q9TUD3
Q9TUD3
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Q9TUD3
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Gapop 10.0 , Gapext 0.5
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
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Match Length
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Seguence:
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Maximum DB :
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LGNQMGEYATLFALARMNGRLAFTPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120

23 61

Dp Qγ qq Ö

WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180

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MEDLINE=98342056; PubWed=9675030;
MEDLINE=98342056; PubWed=9675030;
Sherwood A.L., Holmes E.H.;
"Cloning and expression of the catalytic domain from rat hepatoma H35 cell GDP-fucose: GMI alpha 1-->Zfucosyltransferase, an enzyme which is activated during early stages of chemical carcinogenesis in rat
                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 20, Last sequence update)
01-MAR.2002 (TrEMBLrel. 20, Last annotation update)
Alpha 1,2 fucosyltransferase (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
143 WMEBRYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 202
                                     240
                                                 203 PSTFVGVHVRRGDXVHVMPNVWKGVVADRGXLEKALDMFRARYSSPVFVVTSNGMANCRE 262
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                                                                                                                                          126 YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.7%; Score 1896; DB 11; Length 353; 100.0%; Pred. No. 2.1e-164; Ive . 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               609D64EB222C9585 CRC64;
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hes 353; Conservative
                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Rattus norvegious (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 354;
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                                                                                                                                                                                                                                                                                     Society Many B., Koda Y., Kimura H.;
"Two distinct rat GDP-L-fucose:b-D-galactoside 2-a-L-fucosytytransferase genes.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB006138; BAA21742.1;
InterPro; IPR002516; GT_11.
FP0151; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
SEQUENCE 354 AA; 39995 MW; 8636444888215BA1 CRC64;
                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha 1,2-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha 1,2-fucosyltransferase B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.2%; Score 1772; DB 11;
100.0%; Pred. No. 4.2e-153;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
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Best Local Similarity 100.(
Matches 331; Conservative
PRELIMINARY;
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Eukaryota; Metazoa; Cho
                                                                                                                                                                                                                                                                           TISSUE=COLON CANCER;
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Q9R275;
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Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                               263 NINASRGDVVPAGNGIBGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 322
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                                                                                                                                                                                                Domino S.E., Zhang L., Lowe J.B.;
"Molecular Cloning, Genomic Mapping, and Expression of Two Secretor Blood Group alpha (1,2)Fucosyltransferase Genes Differentially J. Biol. Chem. 276:23748-23756(2001).

EMBL; AF214656; AR45146-1;
                                                                                                                                                                                                                                                                                                  143 WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                   WMEERYRHIPGHFVRFTGYPCSWTFYHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ
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Bureau V., Marionneau S., Cailleau-Thomas A., Le Moullac-Vaidye
                                                                                                                                                           0;
          Liehr T., Le Pendu J.;
"Comparison of the three rat GDP-L-fucose: beta-D-galactoside alpha-L-fucosyltransferases FTA, FTB and FTC.";
Eur. J. Biochem. 268:1006-1019(2001).
EMBL; AF131238; AAD24469.1;
InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferaes; Transferaes.
SEQUENCE 354 AA; 39983 MW; 123EBC8379E8559E CRC64;
                                                                                                                                    354;
                                                                                                                              92.0%; Score 1767; DB 11; Length 11arity 99.7%; Pred. No. 1.2e-152; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD5F441046CC8E79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha(1,2)fucosyltransferase FUT2 (EC 2.4.1.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 AA
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InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycosyltransferase; Transferase
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                                                                                                                                                          330;
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Best Local (
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Q9JL27;
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61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 WMEERYRHIDGOYVRPIGYPCSWIFYHHLRPEILKEFTLHDHYREEAOAFLRGLRYNGSO 195
                                                                                                                                                                                                                                                                                       121 WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPBILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                              136 WMEERYRHIPGQYVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLKGLRVNGSQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                                         PSIFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
                                                                                                                                             LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 NINTSLGDVVFAGNGIEGSPAKDFALLTOCNHTIMTIGTFGIWAAYLAGGDTIYLANYTE 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "GDP-fucose: beta-galactoside alphal, 2-fucosyltransferase, MFUT-II,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and not MFUT-I or III, is induced in a restricted region of the digestive tract of germ-free mice by host-microbe interactions and cycloheximide.";
                                  IGNQMGEYATLFALARMNGRLAFIPESMHNALAPIFRISLPVLHSDTARRIPWQNYHLND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 PSTFVGVHVRRGDYVHVMPKVWKGVVADRGYLEKALDRFRARYSSPVFVVTSNGMAWCRE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBL_TaxID=10090;
STIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
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STRAIN-FOR: TISSUE-GASTROINIESTINAL TRACT;
MEDILNE-20471982: PubMed=11018479;
Lin B., Hayashi Y., Saito M., Sakakibara Y., Yanagisawa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      616CCB11581C4179 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 AA.
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EMBL; AF064792; AAC16887.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
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InterPro: IPR002516; GT_11.
Pfam. PF01531; GIYO_Lransf_11; 1.
GlyCosyltransferase; Transferase.
SEQUENCE 347 AA; 39215 MW; 6160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Q920W3
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            181 PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
                                       241 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus spicilegus (Steppe mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10103;
                                                                                                                                                                                                                                                                                                               Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N. "Conspicuous Differences among Gene Genealogies of 21 Nuclear Gen
Five Mus musculus subspecies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            78.5%; Score 1508.5; DB 11; Length 321; 89.1%; Pred. No. 3.7e-129;
                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Indels
                                                                                                                                                                                                                                                                                                                                    Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB039123; BAB68647.1; -.
FITALPROS PRO02516; GT_11.
Pfam: PF01531; Glyco_Lransf_11; 1.
Glycosyltransferase; Transferase.
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36560 MW; 5B7D19BA6D4B5394 CRC64;
                                                                                                                                                         321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
                                                                                          PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                                                         PRT;
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                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                    2.4.1.69) (Fragment)
FUT2.
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321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity
285; Conserv
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NON_TER
SEQUENCE
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Best Local S:
Matches 285
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Q920W2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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STRAIN=VARIOUS STRAINS;
Liu Y., Kitano T., Kolde T., Shiroishi T., Moriwaki K., Saitou N.;
Liu Y., Kitano T., Kolde T., Shiroishi T., Moriwaki K., Saitou N.;
Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes (Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
6DP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase (EC
FUT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 321;
                            031VF0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLREL) 21, Last annotation update)
(BP-L-fucose: Deta-D-galactoside 2-alpha-1-fucosyltransferase
(BC 2.4.1.69) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

REMEL, AB039114; BAB68638.1; --

EMBL, AB039115; BAB68640.1; --

EMBL, AB039117; BAB68640.1; --

EMBL, AB039118; BAB68641.1; --

EMBL, AB039118; BAB68643.1; --

EMBL, AB039119; BAB68644.1; --

EMBL, AB039121; BAB68644.1; --

EMBL, AB039121; BAB68644.1; --

EMBL, AB039121; BAB68645.1; --

EMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 1508.5; DB 11;
; Pred. No. 3.7e-129;
12; Mismatches 17; I)
         AA
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321
    PRT;
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NON_TER 121
NON TER 321
SEQUENCE 321 AA; 36516 MW; 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.5%;
88.8%;
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Matches 284; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Gaps

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181 PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
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                                                                                                                                                                                                                                                   LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIFWQNYHLND 120
                                                                                                                                                                                                                                                                                                                  WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 NIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTL 311
                                                                                                                                                                                    1 STITHLQQRIVKLQPLSEKELPMITQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 STIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 STIFHVQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGWWTINAIGR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Evolution of alpha2-Fucosyltransferase genes in primates: relation between an intronic Alu-Y element and red cell expression of ABH antigens.";
                                                                                                                                                                                                                                                                                                                                                                                                      72 IGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITILPVLHSATASRIPWQNYHLND
                                                                                                                                                                                                                                                                                                                                     Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                   DB 6; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.8%; Score 1418.5; DB 6; Length 338; 79.5%; Pred. No. 6.4e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20198794; PubMed=10723735;
Apoil P.-A., Roubinet F., Despiau S., Mollicone R., Oriol
Blancher A.;
                                                                                                                74.0%; Score 1421.5; DB 6; Length: 79.8%; Pred. No. 3.5e-121; tive 25; Mismatches 31; Indels
                                                                                     894E28BD74AE8FBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 AA; 38428 MW; E7FABA0FF1BC95F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
J. Biol. Chem. 270:4640-4649(1995).
EMBL; AB015635; BAA31128.1; -.
InterPro; IPR002516; GT_ll.; -.
Pfam. PF01531; G1yco_transf_ll; 1.
G1ycosyltransferase; Transferase.
SEQUENCE 343 AA; 38973 MW; 894E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOl. Biol Evol. 17:337-351(2000).
EMBI, AF080604; AF141066.1; -.
Interpro: IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
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                                                                                                                Query Match
Best Local Similarity 79.8'
Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                Liu Y., Kitano I., Koide T., Shiroishi T., Moriwaki K., Saitou N.; "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.;

"The old origin of a null allele se428 of the human ABO-secretor type
alpha(1,2) fucosyltransferase gene (FUT2).";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95181460; PubMed=7876235; Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.; "Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucosyltansferase gene (FUT2).";
                                                                                                                                                                                                                                                                                                                                                                                 1 STIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
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                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotā, Metazoā, Chordata; Craniata; Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                  7:
                                                                                                                                                                                                                                                                                                                    DB 11; Length 321;
                                                                                                                                                                                                                                                                                                                                                    18; Indels
                                                                                                                                                  Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB039122; BAB68646.1; -.
Inter Prop. is 187005.16; GT_11.
Pfam: PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
                                                                                                                                                                                                                                                                                   321 AA; 36464 MW; FF5304CD150F774A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NVV-1998 (TrEMBLrel. 08, Created)
01-NVV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                77.7%; Score 1493.5; DB 1
88.1%; Pred. No. 8.7e-128;
live 13; Mismatches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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FUT2.
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                                                                                                                                                                                                                                                                                                                                Best Local Similarity 88.18
Matches 282; Conservative
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                                                                                 SEQUENCE FROM N.A.
                                                   NCBI_TaxID=10090;
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                                                                                                  STRAIN-NJL/MSF;
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NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
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                                                                                                                                                                                                                                                   NCBI_TaxID=9593;
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Matches 263;
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Q29505;
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"The old origin of a null allele sed58 of the human ABO-secretor type
alpha(1,2) fucosyltransferase gene (FVT2).";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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             180
                                                          LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                          NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-518146; PubMed=7876235; Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.; Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.; Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucosyltansferase gene (FUT2)."; BMBL; AB015634; BAA31127.1; Interpro: 1PR002516; Gr_ll.
Interpro: IPR002516; Gr_ll.
Glycosyltransferase; Transferase.
SEQUENCE 343 AA; 38999 WW; B849D7E152852081 CRC64;
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                                                                                                          WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ
                                                                                             PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.8%; Score 1418.5; DB 6; Length 79.5%; Pred. No. 6.5e-121; ive 27; Mismatches 30; Indels
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                           343 AA
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Alpha(1,2)fucosyltransferase.
FUT2.
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Best Local Similarity 79.5
Matches 263; Conservative
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181 PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Evolution of alpha2-Fucosyltransferase genes in primates: relation between an intronic Alu-Y element and red cell expression of ABH antigens."
Mol. Biol. Evol. 17:337-351(2000).
EMBL; AF080606; AAF14068.1; '...
InterPro; IPR002516; GT_11.
Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 AA; 39001 MW; A753375D47AE8C8C CRC64;
                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.8%; Score 1417.5; DB 6; 79.5%; Pred. No. 8.1e-121; iive 26; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
                                                                                                                                                                                                                                     343 AA
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                                                                    301 PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ALEXIS;
MEDLINE=20188794; Pubmed=10723735;
                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last
01-MAR-2002 (TrEMBLrel. 20, Last
Alpha (1,2) fucosyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                          Gorilla gorilla (gorilla)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                        Hitoshi S., Kojima N., Kanazawa I., Tsuji S.;

"Molecular cloning and expression of a third type of rabbit GDP-L-
"Molecular cloning and expression of a third type of rabbit GDP-L-
"Lucose:beta-D-galactoside 2-alpha-L-fucosyltransferase.";

J. Biol. Chem. 27:16975-16981(1996)

-!- FUNCTION: CREATES A MEMBRANE-ASSOCIATED PRECURSOR OLIGOSACCHARIDE
FUC-ALPHA((1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN
ESSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE MEMBRANE-ASSOCIATED
A AND B ANTIGEN SYNTHESIS PATHWAY. H AND SE ENZYMES FUCOSYLATE IHE
SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.

-!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + BETA-D-GALACTOSYL-R = GDP +
ALPHA-L-FUCOSYL-1, 2-BETA-D-GALACTOSYL-R = GDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: ADULT GASTROINTESTINAL TRACT AND COLON.
-!- MISCELLANEOUS: THERE ARE THREE GENES (FUT1, FUT2 AND FUT3) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE IN RABBIT. THEY ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STITHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Galactoside 2-L-fucosyltransferase 3 (EC 2.4.1.59) (Secretor blood
group ALPH-12-fucosyltransferase) (GDP-L-fucose:beta-D-galactoside
2-ALPHA-1-fucosyltransferase) (ALPHA(1,2)FT) (Fucosyltransferase 3
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: GLYCOSYLATION.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

746F7007309862A5 CRC64;
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SIMILARITY: STRUCTURAL SIMILARITY WITH THE OTHER MAMMALIAN GLYCOSYLTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.5%; Score 1412.5; DB 6; Length 347; 79.8%; Pred. No. 2.3e-120; tive 25; Mismatches 35; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfan, PF01531; Glyco_transf_11; 1.
Transferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORM IN TRANS CISTERNAE OF GOLGI.
                                                                                                                                                                                                          MEDLINE=96279281; PubMed=8663168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39469 MW;
                                                                                                                                                                                         TISSUE=GASTROINTESTINAL TRACT
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InterPro; IPR002516; GT_11.
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DOMAIN 1 5
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347 AA;
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                                                                                                                               NCBI_TaxID=9986;
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CARBOHYD
CARBOHYD
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Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.;

"The old origin of a null allele se428 of the human ABO-secretor type
alpha(1.2) fucosyltransferase gene (FUT2).";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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EMBL, ABO15636; BAA311291.
InterPro. IPR002516; GI_11.
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                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.4%; Score 1410.5; DB 6; Length 79.2%; Pred. No. 3.5e-120; ive 27; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfan; PF01531; Glyco_transf_11; 1.
Glycosyltransferase: Transferase.
SEQUENCE 343 AA; 38973 MW; 28D4D2A9704E4A0C CRC64;
                                                                08, Created)
08, Last sequence update)
20, Last annotation update)
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                                   PRT;
                                                                                                                   Alpha(1,2) fucosyltransferase.
                                                                                                                                                     Pongo pygmaeus (Orangutan).
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hes 262; Conservative
                                   PRELIMINARY;
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                                                                01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                            - nucleic search, using sw model
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Database

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CIGICCCCACTCCTTAAGGCATTAACACCAGCCTGTCCTCGGTCCCACTTCCACCTCAAG 1020
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Sherwood, A.L., Stroud, M.R., Levery, S.B. and Holmes, E.H.
An amino acid region at the N-terminus of rat hepatoma alphal-->2
fucosyltransferase modulates enzyme activity and interaction with
libids: strong preference for glycosphingolipids containing
terminal Galbetal-->SalaNAc-structures
Biochemistry 40 (19), 5708-5719 (2001)
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2 (bases 1 to 1149)
Sherwood,A.E. and Holmes,E.H.
Direct Submission
Submitted (05-MAY-2000) Molecular Medicine, Northwest Hospital,
                                                                                                                            GTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCT
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Rattus norvegicus alpha 1-2 fucosyltransferase mRNA, complete
AF264005
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Sciurognathi; Muridae; Murinae;
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/cell_line="Reuber H35
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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SHFHLKARGVTCYVAGRAF"
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                                                                                                                       Direct Submission
Submitted (13-79A-1999) Cell Surface Biochem., Northwest Hospital,
120 Northgate Plaza, Suite 230, Seattle, WA 98125, USA
Location/Qualifiers
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H35 cell GDP-fucose:GMI alpha 1-->2fucosyltransferase, an enzyme which is activated during early stages of chemical carcinogenesis
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Arch. Biochem. Biophys. 355 (2), 215-221 (1998)
98342056
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                                                                                           2 (bases 1 to 1068)
Sherwood, A.L. and Holmes, E.H.
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ROD 09-NOV-2001

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us-10-040-863-9.rge

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GIEGSPAKDFALLTQCNHIIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPE
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Direct Submission
Submitted (25-FEB-1999) INSERM U419, Institut de Biologie, 9 Quai
Moncousu, Nantes 44035, France
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Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                      1042 CTGTCCCCACTCTTAAGGCATTAACACCAGCCTGTCCTCGGTCCCACTTCCACCTCAAG
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(FIB) gere,
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Liehr, T. and Le Pendu, J.
Comparison of the three rat GDP-L-fucose:beta-D-galactoside
2-alpha-L-fucosyltransferases FTA, FTB and FTC
Eur. J. Biochem. 268 (4), 1006-1019 (2001)
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/protein_id="AAD24469.1"
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/organism="Rattus norvegicus"
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YPCSWTFYHLIRPELLKEFTLHDHYREEAQAFLRGLRVNGSOPSTFVGVHVRRGDYVH
YPNWWWGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAMCRENINASRGDVVFAGN
GIEGSPBARDFALLFOCHTIPYTIGTFGIMAAYLAGGDTIYLANYTLFDSSPELKVFKPE
AAFLPEWVGIPADLSPLLKH"
ROD 05-FEB-1999
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MTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGR
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Submitted (04-AUG-1997) Yoshiro Koda, Kurume University, School of
Submitted (04-AUG-1997) Yoshiro Koda, Kurume University, School of
Medicine, Department of Forensic Medicine; Asahimachi 57, Kurume,
Fukuoka 810, Japan (E-mail:ykoda@med.kurume-u.ac.jp,
Tel:0942-31-754, Fax:0942-31-7700)
Location/Qualifiers
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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               Rattus norvegicus FTB mRNA for alpha 1,2-fucosyltransferase, complete cds.
AB006138
                                                                                      AB006138.1 GI:2317265
FTB: alpha 1,2-fucosyltransferase.
Rattus norvegicus colon cancer cell_line:RCN-9 cDNA to mRNA.
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/protein_id="BAA21742.1"
/db_xref="G1:2317266"
                                                                                                                                                                                                                                                                                        Soejima,M., Wang,B., Koda,Y. and Kimura,H.
Two distinct rat GDP-L-fucose:b-D-galactoside
2-a-L-fucosyltransferase genes
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Pred. No. 2.9e-266;
); Mismatches 2;
mRNA
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
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/tissue_type="colon cancer"
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/gene="FTB"
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Rattus norvegicus clone CH230-309A14, *** SEQUENCING IN PROGRESS AC1212111
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Muzny, D.M., Adans,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
                                                                                                                    GTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCT
GGTGTCCATGTGCGCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTGAAGGGCGTG
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                                                                                                     TACCGCCACATTCCGGGACACTTTGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTC
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                                            1021 GCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTCTGATGGGAA 1068
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Rattus norvegicus.
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Worley,K.C.

Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Modecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 19, 2002 This sequence version replaced gi:20806241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Pirap: version 0.990329 Consensus quality: 106837 bases at least Q40 Consensus quality: 113151 bases at least Q30 Consensus quality: 116417 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Pred. No. 5.9e-263;
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CTACCACCACCTGCGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGA 479

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YHHLRPEILKEFTLHDHVREERQAFLKGLRYNGSOPSTFYGYHYRGYVYHYRKYNK
GYVADRGYLEKALDRFRARYSSPVFVYTSNGMAMCRENINTSLGDVYFAGNGIBESPA
KDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKIFKPAAAFLPEW
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MHNALAPIFRISLPYLHSDTARRIPWQNYHLNDWMEERYRHIPQQYVRFTGYPCSWTF
                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQTLSEKELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /BC_number="2.4.1.69"
/note="fucosyltransferase; similar to the Mus musculus fratain ICR Sec2 sequence deposited at Genbank Accession Number AF06492; similar to the Homo sapiens secretor blood group alpha(1,2)fucosyltransferase FUT2 sequences deposited at GenBank Accession Numbers D87942 and U17894"
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2210. 3253
/gene="Fut2"
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/protein_id="AAR45146.1"
/db_xref="GI:7288505"
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Pred. No. 9.2e-215;
....trhes 93;
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            Ann Arbor, MI 48109-0650,
Location/Qualifiers
                                                                                                            /map="23.2; between Klkl ar
/cell_line="E14"
/cell_type="E5"
/cell_type="E5"
/gene="Fut2"
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                                      1. .6762
/organism="Mus musculus"
                                                                 /strain="129/0la"
/db_xref="taxon:10090"
/chromosome="7"
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/gene="Fut2"
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Domino,S.E., Zhang,L. and Lowe,J.B.
Molecular cloning, genomic mapping, and expression of two secretor blood group alpha (1,2)fucosyltransferase genes differentially regulated in mouse uterine epithellum and gastrointestinal tract J. Eiol. Chem. 276 (26), 23748-23756 (2001)
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Domino, S.E. and Lowe, J.B.
Direct Submission
Submitted (13-DEC-1999) HHMI, University of Michigan, 1150 W. Med.
                                                                                                                                                                                                                                                                                                                                                                                               GGGTGTCCATGTGCGCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTGGAAGGGCGT
                                                                                                                  GGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCCACGCTATTCATC
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                                            2 (bases 1 to 6762)
Domino,S.E. and Lowe,J.B.
Mus musculus alpha(1,2)fucosyltransferase FUT2 (Sec2) genomic
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121 AATGGAGAGCTGCGGGGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATG 180
                                                          Consensus quality: 191947 bases at least 040
Consensus quality: 197212 bases at least 030
Consensus quality: 198261 bases at least 020
Estimated insert size: 236210; agarose-fp estimation
Estimated insert size: 199546; sum-of-contigs estimation
Conality coverage: 7.3 in 020 bases; agarose-fp estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct a given, however the sizes
* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CICCAGCAGCGAATAGTGAAGCTCCAACCCCTGTCAGAGAAGGAATTACCGATGACGACT
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                                                                                                                                                                                                                                                                                                 * provided by the submitter.

* This sequence will be replaced

* This sequence will be replaced

* the accession number will be preserved.

* 16257 16256 contig of 16256 bp in length

* 16257 38024 contig of 16256 bp in length

* 16357 38024 contig of 22355 bp in length

* 38025 38124 contig of 22335 bp in length

* 58025 38124 contig of 22335 bp in length

* 60460 60589 contig of 22335 bp in length

* 60560 66982 contig of 623 bp in length

* 60560 66982 contig of 623 bp in length

* 60560 106953 contig of 633 bp in length

* 106954 107053 gap of unknown length

* 107054 11366: contig of 4313 bp in length

* 111467 113014 contig of 1848 bp in length

* 111467 113014 contig of 1548 bp in length

* 111467 113014 contig of 1548 bp in length
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52711 c 50595 g 48057 t 1301 others
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g of 1548 bp in length
f unknown length
g of 4877 bp in length
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196982: gap of unknown length
200146: contig of 3164 bp in length.
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of 1835 bp in length
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ilarity 89.3%; Pred. No. 9.1e-215;
Conservative 0; Mismatches 93;
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/organism="Mus musculus"
        Center clone name: RPCI-23_36F17
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/clone="RP23-36F17"
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Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:8810391.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                   541 GGTGTCCATGTGCGCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTGGAAGGGCGTG
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HTG; HTGS_PHASE2; HTGS_DRAFT
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DOE Joint Genome Institute.
Sequencing of Mouse
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DOE Joint Genome Institute.
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21; Gaps

Length 200145;

| Iwamori,M.  GDP-fucose: beta-galactoside alphal,2-fucosyltransferase, MFUT-II, and not MFUT-I or -III, is induced in a restricted region of the disestive tract of germ-free mice by host-microbe interactions and cycloheximide JOURNAL Biochim. Biophys. Acta 1487 (2-3), 275-285 (2000)  MEDLINE 20471982 PUBMED 11018479 REFERENCE 2 (bases I to 1044) ATTHORS Lin,B., Havashi,Y., Salto,M., Sakakihara,Y., Yanagisawa,M. and | <pre>Iwamori,M. Iwamori,M. Direct Submission Submitced (12.84x-1998) Chemistry, Faculty of Selence 5 Tec Kinki University, Kowakae, Higashi-osaka 577-8502, Japan Location/Qualifiers</pre> | /strain="ICR" /db_xref="taxon:10090" /tissue_taxon:10090" /tissue_type="gastrointestinal tract" 1. 1044 /EC_number="2.4.1.69" /rode="sec2; Se" /codon_start=1 /product="gdp-1-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase" | /protein_id="AAĈ16897.1"  /db_xafe=[G1:3142768]  /translation="MASAQVPESPLAHELIFVFVTSTIIHLQQQIVKLQTLSEKELQ AVOMSSPNAARTDMQOSAKLOGIFTINSIGRLGNOMGEYATLFALARANGRLAFITES ANGMALAPIFRISISLEVLHSCDFRRIPMQVATBINDMWEDRYAHIGQGVVRFTGYPGSTOGSTF YHHLRPEILKEFTLHDHVREEAQAFLRGLRANGSQPSTFVGVHVRRGDYHVWPRVWK GVVADRGYLEKALDRERARXSSPVFVTSNOMAMORENINYSLGDVYFAGNGIEGSVB MGIPALIQCONTINTIGTEGIWAAYLAGGDTIYLANYTLFDSPFLKIFKPAAAFLPEW AGIPALDSPLIKH"  BASE COUNT 229 a 318 c 271 q 226 t   | / Match 74.1%; Scor<br>Local Similarity 89.9%; Pred<br>Nes 879; Conservative 0; M   | QY 1 CTCCAGCAGCGAATAGTGAAGCTCCAACCCCTGTCAGGAAGGA | Qy   61 CAAATGTCCTCGGGAAACACAGAAGATGCGACGGGACAGCGAGCAGCGGGGCTCGG 120 |  | 0y         241 GCATCCATGCACAACGCTCTAGCGCTCTCAGGATCAGCTTCCCGGTGTTACAGGC 300           bb         111111111111111111111111111111111111   |
|---|---|---|---|---|--|--|--|--|
| 13777 GGCGAATATGCTACACTGGCCAGGATGAACGGTCGGCTTGCCTTCATCCCT 241 GCATCCATGCACACACTTAGGGCCCATCTTCAGGATCAGCCTCCGGGTGTTACACACGCT 13717 GAATCCATGCACACACGCTCTAGGGCCCATCTTCAGGATCAGCTTCCCGGTGTTACACAGC 301 GACAGGCCAAAAAGGTCCCATGGCAGAATTACCATCTCAACGACTGGATGGA   | Qy         351 TACGCCACAATTCGGGGACATTCTGGGGTTCAGGGATACCCGTGCTCCTGGACCTC         420           111111111111111111111111111111111111  | 481 GAGGCCGAGGCCTTCCTGCGTGGTCTGCGGTGAATGGGAGCCAGCC  | UNIVERSE   UNIVERSE | 781 CIGCTCACCCAGTGCAACCACCATCATGGACTATTGGGACCTTTGGGATTTGGCACCCAGTGCAACGATTTGGCACCTTTGGGATTTTTGGATTTTTGGATTTTTGGATTTTTGGATTTTTGGATTTTTGGATTTTTGGATTTTTT | 841  | 0.0   0.0   CTCAAAGTCTTTAAGCCAGAGGAGCCTTCCTACCGAATGGGTGGG            | Oy 1021 GCAAAAGGAGTCACTTGTTACGTCGCAGGAGAGCCTTCTGATGGGAA 1068<br> | RESULT 8 AF064792 LOCUS DEFINITION Mus musculus GDP-L-fucose:Deta-D-galactoside 2-alpha-1-fucosyltransferase mRNA, complete cds. ACCESSION AF064792 |

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us-10-040-863-9.rge

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/EC_number="2,4.1.69"
/note="Sec2; Se"
                                                                            /codon_start=1
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89.9%;
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/gene="FUT2"
1. .963
/gene="FUT2"
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Mus musculus (sub_species:domesticus, strain:C57BL/10SnJ) DNA.
Mus musculus
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Liu, Y. and Saitou, N.
Direct Submission
Submitted (29-FEB-2000) Naruya Saitou, National Institute of
Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Mishima,
Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp,
URL:http://sayar.lab.nig.ac.jp/, Tel:81-559-81-6790,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus FUT2 gene for GDP-L-fucose; beta-D-galactoside
2-alpha-1-fucosyltransferase, partial cds, strain:C57BL/10snJ.
AB039114
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Acc#AF064792"
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/db_xref="taxon:10090"
/chromosome="7"
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of Five Mus musculus subspecies
Unpublished
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/product="GDP-L-fucose:beta-D-galactoside
2-alpha-1-fucosyltransferase"
2-alpha-1-fucosyltransferase"
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HDHVREEAQAFLRGLANVGSOPSTFVGYHVRRGDYVHVMFKWWRGYAALREFALL
RFRARYSSPVFVVTSNGMAWGRENINTSLGDVVFAGNGIEGSPAKDFALLTQCNHTIM
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Pred. No. 2.2e-190;
0; Mismatches 74;
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HDHYREEAQAFLRGLRVNGSQPSTFVGVHYRRGDYVHVMPKVWKGYVADRGYLEKALD
RFRARYSSPVFVTSNGMAMCRENINTSLGDVVFAGNGIEGSPAKDFALLTQCNHTIM
TGFFGIWAAYLAGGDTAANYTLPDSPFLKIFKPAAFLPEWM"
285 0 207 t
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Mus musculus FUT2 gene for GDP-L-fucose:beta-D-galactoside
2-alpha-1-fucosyltransferase, partial cds, strain:BFM/2Msf.
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QQSAKLQGIFTINSIGRLGNQMGEYATLFALARMNGRLAFIPESMHNALAPIFRISLP
                                                                                                                                                                                                                                                                                                    AB039115.1 GI:15822975
FUT2; GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase.
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                                                                                                             Submitted (29-FEB-2000) Naruya Saitou, National Institute of Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Mishima, Shizuoka 411-8540, Japan (E-mall:nsaitou@qenes.nig.ac.jp, URL:http://sayar.lab.nig.ac.jp/, Tel:81-559-81-6790, Fax:81-559-81-6789)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
CTGCTCACCCAGTGCAACCACCATCATGACTATTGGGACCTTTGGGATTTGGGCTGCC
                                                                                               TACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTACACCGTTCCGGGATTCTCCGGTTC
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                                                                                                                                                                    /product="GDP-L-fucose:beta-D-galactoside
-2-alpha-1-fucosyltransferase"
/protein_id="Bab68639.1"
/db_xref="G1:15822976"
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Pred. No. 2.2e-190;
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/db_xref="taxon:10090"
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Acc#AF064792"
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/strain="BFM/2Msf"
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/EC_number="2.4.1.69"
/note="Sec2; Se"
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1. 963
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2 (bases 1 to 963)
Liu,Y. and Saitou,N.
Direct Submission
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Mus musculus FUT2 gene for GDP-L-fucose; beta-D-galactoside
2-alphal-fucosyltransferase, partial cds, strain:BLG2/Msf.
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                         1 CICCAGCAGATAGTGAAGCTCCAACCCCTGTCAGAGAAGGAATTACCGATGACGACT
                                                                              61 CAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGACGGGACAGCGAGCAGCATGGG
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Location/Qualifiers
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QOSAKLQGIFTINSIGRLGONGGETARTÉALARMORIALEIPESMHNALAPIFRISLP
VLASOTARRIPWONRELNDMEERYHIPGOVVRFOSYPCSWTFVHLRPEILKEFTL
HDHVREBAQAFIRGLRVNGSQPSTFVCVHVRRGDYVHVMPKVWKGVVADRGYLEKALD
HFRARKSSPYFVYTSWGMAMQRENINNSLGDVVFAGNOIBGSPAKDFALLTQCNHTIM
TIGTEGINAAVLAGGONACRENINNSLGDVFFAGNOIBGSPAKDFALLTQCNHTIM
TIGTEGINAAVLAGGONACRENINNSLGDVFFAGNOIBGSPAKDFALLTQCNHTIM
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                                                                                                                                                                            liu, Y. and Saitou, N.

Direct Submission

Submitted (199-FFB-2000) Naruya Saitou, National Institute of
Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Mishima,
Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp,
URL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AATGGAGAGCTGCGGGGCATGTTCACGATCCAATTCCATTGGCCGGCTGGGGAACCAGATG 180
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Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes
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                                                                          Mus
                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                      Liu, Y., Kitano, T., Koide, T., Shiroishi, T., Moriwaki, K. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.6%; Score 764.6; DB 10; Length 963; 89.9%; Pred. No. 2.2e-190;
                                                                                                                                                                                                                                                                                                                                                                                                           primer design based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="GDP-L-fucose:beta-D-galactoside
2-abpha-1-fucosyltransferase"
/protein_id="aba68640.1"
/db_xref="G1:15822978"
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/note="sequence used for
Acc#AF064792"
                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                            /sub_species="musculus"
/db_xref="taxon:10090"
                                                                                                                                                  of Five Mus musculus subspecies
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="FUT2"
/EC_number="2.4.1.69"
/note="Sec2; Se"
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .963
                                                                                                                                                                                                                                                                                                                                             /strain="BLG2/Msf"
GI:15822977
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                                             Mus musculus
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Matches
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AB039117
Mus musculus FUT2 gene for GDP-L-fucose;beta-D-galactoside
2-alpha-1-fucosyltransferase, partial cds, strain:CAST/Ei.
AB039117
AB039117. GI:15822979
FUT2; GDP-L-fucose;beta-D-galactoside 2-alpha-1-fucosyltransferase.
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Liu, Y. and Saitou, N.
Direct Submission
Submitted (29-FBB-2000) Naruya Saitou, National Institute of
Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Mishima,
Shizuoka A11-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp,
URL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790,
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                                                                         859 TACCTGGCAGGTGGTGATACCATCTACCTAGCCAACTACACCTTCCGGATTCTCCGTTTC
  TACCGCCACATTCCGGGACACTTTGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTC
                                                                                                                                                 TACCACCACCTGCGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAG
                                                                                                                                                                          541 GGTGTCCATGTGCGCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTAAGGGGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GIGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/translation="Filfveyvistiihloorivklotusekeloavomsspnaartdm
QQSAKLQGIFFIINSIGRLGNOMGEYATLFALARWNGRLAFIPESMHNALAPIFRISLP
VLHSDTARRIPWQNYHLNDWMEERYRHIPGQYVRFTGYPCSWTFYHHLRPEILKEFTL
HDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDXVHVMPKVWKGVVADRGYLEKALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB039118.1 GI:15822981
AB039118.1 GI:15822981
FUT2; GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase.
Mus musculus (sub_species:molossinus, strain:MSM/Msf) DNA.
Mus musculus
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Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes
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Diu,Y. and Saitou,N.
Diu,Y. and Saitou,N.
Submitted (29-FBB-2000) Naruya Saitou, National Institute of Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Mishima, Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp, URL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
619 GTGGCTGACCGGGGTTACCTAGAAAAGGCCCTGGACAGGTTCCGGGCACGCTATTCATCT
                                                          CTAGGAGACGTGGTGTTTGCGGGCAATGGTATTGAGGGCTCACCAGCCAAGGACTTCGCG
                                     CCAGTCTTCGTGGTTACAAGGAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCC
                                                                                                                                                                                                                                        CTCCTCACCCCAGTGCAACCACCATCATGACCATTGGAACCTTTGGGATTTGGGCTGCC
                                                                                                                    CTGCTCACCCAGTGCAACCACACATCATGACTATTGGGACCTTTGGGATTTGGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus FUT2 gene for GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase, partial cds, strain:MSM/Msf.
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                                                                                                                                                                                                                   /note="sequence used for primer design based
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2-alpha-1-fucosyltransferase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sub_species="molossinus"
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/db_xref="GI:15822982"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Five Mus musculus subspecies Unpublished
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/chromosome="7"
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QQSAKLQGIFIINSIGRLGNQMGEYATLFALARMNGRLAFIPESMHNALAPIFRISLP
VLHSDTARRIPWQNYHLNDWMEERYRHIPGQYVRFTGYPCSWTFYHLRPEIIKEFTL
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RPRARXSSPYVVTGNGMAMCRENINTSLGDVVFAGNGIEGSPAKDFALLTQCNHTIM
TIGTRGIWAAYLAGGDTAANTLEPDSPFLKTFKPAAAFLPEWM"
285 c 257 g 207 c
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                                                                                               /note="sequence used for primer design based Acc*AF064792"
                                                                                                                                                                                                                                                                       /produc_t="GDP-L-fucose:beta-D-galactoside
-2-alpha-1-fucosyltransferase"
/protein.id="RbB68641.1"
/db_xref="G1:15822980"
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Pred. No. 2.2e-190;
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  organism="Mus musculus"
                                       /sub_species="castaneus"
                                                       /db_xref="taxon:10090'
/chromosome="7"
                                                                                                                                                                                                                 /EC_number="2.4.1.69"
/note="Sec2; Se"
                  /strain="CAST/Ei"
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/gene="FUT2"
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                                              Score 764.6; DB 10;
Pred. No. 2.2e-190;
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QQSAKLQGTFINSIGRLGNQMSGPATLFALARMSRLAFTERSHMNATALFIERSHDW
QQSAKLQGTFTINSIGRLGNQMSGPATLFALARMSRLAFTERSHMNATALFIERSLF
VLHSDPARTEPWONTHLNDMNEERYBHIPGOVNFTGYPCSWTFYHLIREFELL
HDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPKVWKGVVADRGYLEKFTL
FERRAKYSSPVTYTSNGMAWCRRINTSLGDVVFAGNOIEGSFAKDFALLTQCNHTIM
FRERAKYSSPVTYTSNGMAWCRRINTSLEDSPELKIFKFAAAFLEBGWM"
1 285 C 257 5 G 77 277
Mus musculus FUT2 gene for GDP-L-fucose;beta-D-galactoside
2-alpha-1-fucosyltransferase, partial cds, strain:pgn2.
AB039119
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F0T2; GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             liu, Y. and Saitou, N.

Direct Submission

Submitted (29-FBB-2000) Naruya Saitou, National Institute of
Genetics, Laboratory of Evolutionary Genetics: 1111 Yata, Mishima,
Shizuoka 471-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp,
URL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-5790,
                                                                                                                                                                                                                                                                                                                                                                                          Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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89.9%; Pred. No. 2.2e-190;
iive 0; Mismatches 74; Indels 21;
                                                                                                                                                                                                                                                                                                                                  Liu,Y., Kitano,T., Koide,T., Shiroishi,T., Moriwaki,K. Saitou,N.
                                                                                                                                                                                                Mus musculus (sub_species:domesticus, strain:pgn2) DNA
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2-alpha-1-fucosyltransferase"
/protein_id="BAB68643.1"
/db_xref="GI:15822984"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="sequence used for primer design Acc#AF064792"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                           of Five Mus musculus subspecies
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/note="Sec2; Se" .
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="pgn2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus FUT2 gene for GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase, partial cds, strain:SWN/Msf. AB039120.
AB039120.
AB039120.
GI:15822985
FUT2; GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase. Mus musculus (sub_species:molossinus, strain:SWN/Msf) DNA.
                                                                                                                                                                                                                                           540
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            258
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                                                                                                                                        GGTGTCCATGTGCGCCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTGAAGGGCGTG
                                                                                                                                                                                                                                                                                                             CTAGGAGACGTGGTGTTTGCGGGCAATGGTATTGAGGGCTCACCAGCCAAGGACTTCGCG
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                                                                                                                                                                                                                                                                                                                                                             CTGCTCACCCCAGTGCACCACCATCATGACTATTGGGACCTTTGGGATTTGGGCTGCC
GCATCCATGCACAACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGC
                                                    CCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostc
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu, Y., Kitano, T., Koide, T., Shiroishi, T., Moriwaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCAAAGICTITAAGCCAGAGGCAGCCTTCCTACCCGAATGGGTG 945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saitou, N.
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199 619 721 739 781 199 841 859 901 919

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of Five Mus musculus subspecies

Unpublished

DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

RESULT 15 AB039120 LOCUS

ORGANISM

REFERENCE AUTHORS 2 (bases 1 to 963) Liu,Y. and Saitou,N. Direct Submission

AUTHORS

REFERENCE

JOURNAL TITLE

QGSAKLQGIFTINSIGRLGNOMGEYATLFÄLARMNGRLAFIPESMHNALAPIFRISLP VLHSDTARRIPWQNYHLNDWMEERYRHIPGQYVRFTGYPCSWTFYHHLRPEILKEFTL HDHVRREAQAFLRGLRVNGSQPSTFVGYHVRRODYNHVMFYWKGVYADRGYLEKALD RFRARYSSPVFVYTSNGMAWCRNINTSLGDVVFAGNGIEGSPAKDFALLTQCNHTIM TGGFGIMAAYLAGGDIYANYTLEDSPFLKIFKKPAAAFLEFEWM" /product="GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase" /protein\_id="BaA66644.1" /db\_xref="GI:\S22996" /translation="FLIFVFVTSTIIHLQQRIVKLQTLSEKELQAVQMSSPNAARTDM 2 240 360 420 498 54 C 300 378 438 480 120 258 of Mishima, 96 AATGGAGAGCTGCGGGCCATGTTCACGATTCCATTGGCCGGCTGGGGGAACCAGATG TACCGCCACATICCGGGACACITIGIGCGCITCACGGGAIACCCGIGCICCTGGACCTIC TACCACCACCTGCGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAG CAAATGTCCTCGGGAAACACACAGAAAGCCCAGAGATGCGACGGGGACAGCGAGCAGCATGGG CTCCAGCAGCGAATAGTGAAGCTCCAACCCCTGTCAGAGAAGGAATTACCGATGACGACT CTCCAGCAACGAATAGTGAAGCTCCAAACCCTGTCAGAGAAGGAATTAC---AGGCGGTT GCATCCATGCACACACACTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGGC Gaps Submitted (29-FEB-2000) Naruya Saitou, National Institute Genetics, Laboratory of Evolutionary Genetics: 1111 Yata, Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp, URL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790, Pax:81-559-81-6789) ö 21; Length 963; /note="sequence used for primer design based / Match 71.6%; Score 764.6; DB 10; Length: Local Similarity 89.9%; Pred. No. 2.2e-190; nes 850; Conservative 0; Mismatches 74; Indels /sub\_species="molossinus" musculus" /db\_xref="taxon:10090" 481 δ q g ŏ

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601 GTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCT 660
                                        721 CGAGGAGACGTGTTCGCGGGCAATGGTATTGAGGGGTCGCCAGGCAAGGACTTCGCG 780
                                                                                                      841 TACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGGTTC 900
541 GGIGICCATGIGCGCCGAGGGGACTAIGIGCAIGTCAIGCCIAAIGIGGAAGGGCGIG 600
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Search completed: May 26, 2003, 14:49:17 Job time: 2883.28 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Human Sec2 coding
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                                                    ; Search time 276.996 Seconds
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                                                             Run on:
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|  | 8 BP.                | 1068 | ; cDNA;    | standard; | 67966          | RESULT 1<br>AAC67966<br>ID AAC67966 |  |
|--|----------------------|------|------------|-----------|----------------|-------------------------------------|--|
|  | ALIGNMENTS           |      |            |           |                |                                     |  |
| Human DNA containi                       | AAH79569             |      | 51         |           | ω.             | 45                                  |  |
| n alphal-2fuc                            | AAC67971             |      |            |           |                |                                     |  |
| Human cons encodin<br>Human polynucleoti | AAS31284<br>ARO66608 | 22   | 3044       | w w       | 40.4           | 0 42                                |  |
| encoding nove                            | ABK43445             |      |            |           | 0.             | •                                   |  |
| a secreted pr                            | AAD05059             |      |            |           |                |                                     |  |
| n secreted pr                            | AAD05087             |      |            |           | 40             |                                     |  |
| Human polynucleoti                       | AAK51656             |      |            |           | 2              | 37                                  |  |
| Human cDNA sequenc                       | AAH17772             |      |            |           | 2              | 36                                  |  |
| Human cDNA clone (                       | AAC6/3/2<br>AAH06199 |      | 100<br>495 |           | υ<br>4         | 3.4<br>3.5                          |  |
| Human alpha1-2fuco                       | AAC67969             |      | 100        |           | m.             | 33                                  |  |
| Human alphal-2fuco                       | AAC67975             |      | 100        |           | . o            | 32                                  |  |
| Rabbit alphal-ziuc<br>Rabbit alphal-Zfuc | AAC6/9/8<br>AAC67981 |      | 100        |           |                | 30                                  |  |
| Rabbit alphal-2fuc                       | AAC67984             |      | 100        |           | ď.             | 58                                  |  |
| Human secreted pro                       | AAC03536             |      |            | ä         | 25.            | 28                                  |  |
| X. laevis alpha-1,                       | AAX77268             |      |            |           | . <del>.</del> | 27                                  |  |
| human alpha(1,2)-1<br>DNA encoding a g-y | AAT61677<br>AAO56908 |      | 8174       |           | 4.0            | 25<br>26                            |  |
| GDP-Fuc;beta-D-gal                       | AAQ13332             |      |            | 7         | $\Box$         | 24                                  |  |
| Chicken beta-actin                       | AAT63575             |      |            |           | 0              | 233                                 |  |
| Human alpha 1,2 fu                       | AAT76768             |      |            | ٠,        |                | 22                                  |  |
| Mouse H2Kb gene pr                       | AAA53820<br>AAT63576 |      |            | ٠,        | 7              | 20                                  |  |
| Human H-transferas                       | AAT12238             |      |            | 7         |                | 19                                  |  |
| 2-Alpha-fucosyltra                       | AAT01083             |      |            |           | 0              | 18                                  |  |
| 2-Alpha-fucósyltra                       | AAU96491<br>AAT01082 |      |            |           | $\neg$         | 1 T                                 |  |
| CODE CONS. SUS SC                        | AA1/2831             |      |            | T. I.     | 23             | 15                                  |  |
| Tbha-T                                   | AAZ94417             |      |            | ·         | 23.            | 14                                  |  |
| alpha.                                   | AAX03811             |      |            | σ.        | 23             | 13                                  |  |
| nent of                                  | AAX15872             |      |            |           | 23.            | 12                                  |  |
| ransi                                    | AAV21640             |      |            |           |                | 110                                 |  |
| Pancreas cancer re                       | ABT.70026            | 77   |            |           | 0              | Ç                                   |  |
|  |                      |      |            |           |                |                                     |  |

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Rat hepatoma H35 cell alphal-2fucosyltransferase catalytic domain cDNA.
                                                                       Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective;
nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAc; immunotherapy;
immunosuppression; cancer; neurological disease;
                                                                                                                                                                                                                                                (PACI-) PACIFIC NORTHWEST CANCER FOUND.
                                                                                                      small cell lung carcinoma; ss
                                                                                                                                                                                                         99WO-US07384
                                                                                                                                                                                    99WO-US07384
                                   (first entry)
                                                                                                                                                                                                                                                 Holmes EH, Sherwood AL;
                                                                                                                                                                                                                                                                    WPI; 2000-687262/67.
P-PSDB; AAB36105.
                                                                                                                           Rattus norvegicus.
                                                                                                                                              WO200064464-A1.
                                                                                                                                                                                     23-APR-1999;
                                                                                                                                                                                                        23-APR-1999;
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                                   19-FEB-2001
               AAC67966;
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 $\alpha$ 

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producing
                                                CICAAAGICITITAAGCCAGAGGCAGCCIICCIACCCGAATGGGTGGGCATCCCIGCCGAI
                                                                                                                                                                                                                                                                                             CIGICCCCACICCIIAAGGCAIIAACACCAGCCIGICCICGGICCCACIICCACCICAAG
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                                                                                                                                                                                              841 TACCTGGCAGGTGGTGATACCATCTACCCAACTACACCCTTCCGGATTCTCCGTTC
                                                                                                                                                                                                                                            CTGCTCACCCAGTGCAACCACCACCATCATGACTATTGGGACCTTTGGGALTTTGGGCTGCC
                                                                                                                                                              TACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; alphal-2fucosyltransferase; alphal-2FucT; antisense therapy; galactose betal-3N-acetylgalactosamine; Galbetal-3GalNAc; glycolipid; glycoprotein; oligosaccharide; fucosyl-GM1; cancer; gene therapy; oncoganic transformation; cytostatic; ganglioside; GM1; cell transformation; catalytic domain; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hepatoma H35 cell alphal-2FucT catalytic domain encoding DNA
                                                                                                                                                                                                                                                                                                                                                          GCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTCTGATGGGAA 1068
                                                                                                                                                                                                                                                                                                                                                                            cell alphal-2FucT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for |
GMI-specific alphal-2fucosyltransferase enzyme by recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "CDS does not include start codon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Rat hepatoma H35
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                                                                                                The present sequence is given in a specification relating to a rat paragralisate de GML specific alphal-Zfucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-Zgalbetal-3GalNac, a glycolipid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising Fucalphal-Zgalbetal-3GalNac. The method involves contacting alphal-Zfucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoprotein, glycolipoprotein or useful for synthesis of fucosyl-GML by contacting the protein with GDP-fucose and ganglioside GML1. The obtained glycoproteins,
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   rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for paration of fucosyl GMI which is useful as a nutritional composition immunotherapeutic for cancer and neurological diseases -
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                                                                                                                                                                                                                                                                                                                                            Sequence 1068 BP; 237 A; 308 C; 300 G; 223 T; 0 other;
                                                                     Fig 3A; 91pp; English.
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Matches 1068; Conserv
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or immunothe
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                                                                                                                                                                                                     (alphal-2Fucr) enzyme and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate moiety found in ganglioside GM1, a terminal galactose betal-3N-acetylgalactosamine (Galbetal-3GalNac) saccharide. Alphal-2Fucr DNA is useful for producing rat alphal-2Fucr protein by recombinant techniques. Alphal-2Fucr DNA is useful for the proparative synthesis of fucosyl containing glycolipids, glycolipids, glycolipids, glycolipids, glycolipids, glycolipids, alphal-2Fucr DNA is useful for detecting oncogenic transformation which involves assaying for changes in expression of alphal-2Fucr Since alphal-2Fucr is activated in cell transformation, antisense sequences derived from alphal-2Fucr DNA are useful for inhibiting, suppressing antisense therapy. The present sequence is rat hepatoma H35 cell alphal-2Fucr catalytic domain encoding DNA.
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techniques and for detecting oncogenic transformation of test tissues
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Matches 1068; Conservative
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                           841 IACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTACACCTTCCGGATTCTCCGGTTC
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                                                                                                                                                                                                                                                                                                                         GCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTCTGATGGGAA 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat hepatoma H35 cell alphal-2fucosyltransferase cDNA
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GDP-fucose and ganglioside GM_1. The obtained glycoproteins, glycolipoproteins, glycolipids and oligosaccharides are useful as nutritional compositions and fucosyl-GM_1 is useful for inducing an immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
                                                                       3; DB 21; Length 1149;
8.9e-289;
                                                      Sequence 1149 BP; 247 A; 341 C; 311 G; 250 T; 0 other;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for producing GMI-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues .
1042 CIGICCCCACITCTIAAGGCATIAACACCAGCCIGICCTCGGTCCCACIICCACCTCAAG
                                                                                                         CTGTCCCCACTCCTTAAGGCATTAACACCAGCCTGTCCTCGGTCCCACTTCCACCTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  galactose betal-3N-acetylgalactosamine, Galbetal-3GalNAc, glycolipid, glycoprotein, glycolipoprotein, oligosaccharide, fucosyl-GM1, cancer, gene therapy, oncogenic transformation, cytostatic, ganglioside, GM1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to rat GMI-specific alphal-2fucosyltransferase
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/note= "Region which overlaps rat
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662..1149
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P-PSDB; AAE16622.
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Pred. No. 2.3e-161;
O: Mismatches 172;
                                                                                                                                  Porcine secretor transferase (FUT2) gene.
                                                                                                                                                                                         Location/Qualifiers 9..1031
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Best Local Similarity 80.6
Matches 716; Conservative
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                                 DB 24; Length 1149;
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                 Sequence 1149 BP; 247 A; 341 C; 311 G; 250 T; 0 other;
                                100.0%; Score 1068; DB 24; 100.0%; Pred. No. 8.3e-289;
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                                                 0; Mismatches
                                         Best Local Similarity 100.
Matches 1068; Conservative
 alphal-2FucT DNA
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                                         Secretor; glycosyltransferase; FUT2; pig; epitope; antigen; transgenic animal; xenotransplantation; organ transplant; ss.
GCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTCTGATGGGAA
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transplantation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes pig secretor used in an example of the present invention. The present invention describes nucleic acids (NA) encoding a chimeric glycosyltransferase. The NAs comprise a catalytic domain of a first glycosyltransferase (GT) and a localisation signal of a second GT, whereby when the NA is expressed in a cell and where the chimeric enzyme is located in an area of the cell where it is able to compete for substrate with a second GT, resulting in reduced levels of a product from the second GT. The NAs can be used to produce cells and organs with desired glycosylation patterns. Products and methods of the present invention can be used to reduce the levels of undesiredally and the second GT, and the levels of undesiredally considered the levels of undesiredally considered the levels of undesirable epitopes in cells, tissues or organs which may be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITCAGGATCAGCCTCCCGGTGTTACACAGGGGCACGGCCAAAAAAAGATCCCATGGCAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACACTCTTTGCACTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 AGGATGAACGGACGGCTTGCGTTCATCCCCGCATCCATGCACACGCTCTAGCGCCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACCATCTCAACGACTGGATGGAGGGGTTACCGCCACATTCCGGGACACTTTGTGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIGACGCAGGCCACAGAGCCCCTCGAGCCCCCAGCTGAAGGGCATGTGGACGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding chimeric glycosyltransferases - used for altering carbohydrate levels on the surface of cells, useful in gene therapy and transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 612.8; DB 19;
Pred. No. 2.3e-161;
0; Mismatches 172;
Location/Qualifiers 9..1031
                                                                        "secretor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transplantation or gene therapy..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Fig 6; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 57.4%;
Local Similarity 80.6%;
hes 716; Conservative
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                                                                                                                                                                                                                             01-AUG-1997;
                                                                                                                                                                                                                                                                           21-AUG-1996;
                                                                                                                          WO9805768-A1
                                                                                                                                                                                                                                                                                                   02-AUG-1996;
                                                                                                                                                                           12-FEB-1998
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Pig; secretor; chimeric; glycosyltransferase; gene therapy;

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128 AGCTGCGGGGCATGTTCACGATCCATTCCATTGGCCGCCTGGGGAACCAGATGGGCGAAT 187
                                                                                                                                        This sequence encodes the human Sec2 protein of the invention. The DNA encodes a alpha(1,2) fucosyltransferase and is the Secretor alpha(1,2)fucosyltransferase locus, that cross hybridises with the H blood group alpha(1,2)fucosyltransferase gene. The DNA is useful for producing a recombinant human GDP-L-fucose.Deta-D-galactoside 2-alpha-Lincosyltransferase (FUT2) which can be used for genotyping an individual as a secretor or nonsecretor as it is known that nonsecretors homozygous for a mutant allele of the FUT2 gene that has a stop codon in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCCCGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    728 ACGIGGIGITCGCGGGCAATGGIATTGAGGGTCGCCAGCCAAGGACTTCGCGCTGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       428 ACCTGCGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAGGAGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               548 ATGIGCGCCGAGGGGACTAIGIGCAIGTCATGCCTAATGIGTGGAAGGGCGTGGTGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 608 ACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  719 ACCGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 ACGCCACACTCTTTGCACTGGCCAGGATGAACGGACGGCTTGCGTTCATCCCCGCATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 TGCACACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGCGACACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 368 ACATTCCGGGACACTTTGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACC
                                                                             recombinant enzyme and genotyping person as secretor or nonsecretor
                                                                                                                                                                                                                                                                                                                                         55.3%; Score 590.6; DB 19; Length 2115; 79.8%; Pred. No. 5e-155;
                                                              useful for producing
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                          Sequence 2115 BP; 505 A; 606 C; 552 G; 452 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 179;
                                                                                                                                                                                                                                                                             the position corresponding to amino acid 143.
                                                              encoding fucosyltransferase enzyme
                                                                                                            55pp; English
                                                                                                                                                                                                                                                                                                                                             Query Match 55.3
Best Local Similarity 79.8
Matches 709; Conservative
                                                                                                              Claim 1; Column 45-50;
            WPI; 1998-520127/44.
                               P-PSDB; AAW69332
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                                                                                                                                                                                                                                                                                                                                                                                                                              ACCATTGGCACGTTCGGGATCTGGGCCCCTACCTTGCTGGAGAGACCATCTACCTG
                                GCCTGGTGTCGGGAAAACATCAATGCCTCGCGCGCGATGTGGTGTTTGCCGGCAATGGC
                                                                                                                                                                                                                                                                                                                                              ATTGAGGGGTCGCCAGCCAAGGACTTCGCGCTGCTCACCCCAGTGCAACCACCACCATCATG
                                                                                                                                                                                                                                                                                                                                                                ACTATTGGGACCTTTGGGGATTTGGGCTGCCTGCCTGGCAGGTGGTGATACCATCTACTTA
                                                                                                                                               CATGTCATGCCTAATGTGGAAGGGCGTGGTGGTGACCGGGGTTACCTGGAAAAGGCC
                                                                                                                                                                              CACGTGATGCCCAACGTGTGGAAGGGCGTGGTGGCCGACCGGCGGTACCTGGAGCAGGCC
                                                                                                                                                                                                               CTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCTTCGTGGTTACAAGCAACGGTATG
                                                                                                                                                                                                                                                                               GCCTGGTGCCGGGAGACATTAATGCTTCCCGAGGAGACGTGGTGTTCGCGGGCAATGGT
               GAGTTCACCCTGCATGACCACGTGCGGGAGGAGGCCCAGGCCTTCCTGCGTGGTCTTGCGG
                                                                               GTGAATGGGAGCCAGCCGAGTACTTTTGTGGGTGTCCATGTGCGCCGAGGGGACTATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTACCCGAATGGGTGGGCATCCTGCCGATCTGTCCCCACTCCTTAAG 978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
64..1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA; 2115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0395800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sec2 coding sequence.
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KELLY R J.
LENNON G.
LOWE J B.
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                    CCTTACTCAA-GCACTAATGCTGGCCGTCCTTTGAGACCTTTTCTCCT 1126
                                                                                                                                       CACTCCTTAAGGCATTAACACCAGCCTGTCCTCGGTCCCCACTTCCACCT 1016
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2000US-237316P.
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABLG1664 comprises a sequence (S) selected from 847 sequences (given in ABLG1664 comprises a sequence (G) activity, and can be used fanti-neoplastic activity. (I) has cytostatic comprises in indicative of anti-neoplastic agent, and can be used for producing a product which can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a crivity and can properties of the agent. MI can be used in the structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, onesophageal, ovarian, kidney, prostate or panceatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating dottal cancer, infiltrating dottal cancer, squamous cell carcinoma, neuroendocrine controlled.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 TGCACAACGCTCTAGCGCCCAICTTCAGGATCAGCCTCCCGGTGTTACACACACGG
                                                                                                                                                                                                                             Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                        Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
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                        2000US-237606P.
2000US-237608P.
2000US-244867P.
2000US-245084P.
2000US-237604P.
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Best Local Similarity 78.79
Matches 704, Conservative
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Query Match
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineophastic; Wilm's tumour; adenocarcinoma;
707 AIGITOGCCGAGGGACTAIGICCAIGTCAIGCCAAAAGTGGAAGGGGGTGGIGGCCG 766
               ACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCT 667
                                                                                       TCGTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCCCGAGGAG
                                                       728 ACGIGGIGIICGCGGGCAATGGTATTGAGGGGTCGCCAGCCAAGGACTTCGCGCTGCTCA
                                                                                                            CCCAGTGCAACCACCATCATGACTATTGGGACCTTTGGGATTTGGGCTGCCTACCTGG
                                                                                                                                                                        TCTTTAAGCCAGAGCAGCCTTCCTACCCGAATGGGTGGGCATCCCTGCCGATCTGTCCC
                         CACTCCTTAAGGCATTAACACCAGCCTGTCCTCGGTCCCACTTCCACCTCAAGGC 1022
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2000US - 234 034 P.
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TSCACAACGCTCTAGCGCCCCATCTTCAGGATCAGCCTCCCCGGTGTTACACAGCGACACGG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (s) selected from 847 sequences (given in ABLE1664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carter KC, Ebner R, Endress G,
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27-SEP-2000; 2000US-235863P.
28-SEP-2000; 2000US-236028P.
28-SEP-2000; 2000US-236032P.
28-SEP-2000; 2000US-236034P.
28-SEP-2000; 2000US-236110P.
29-SEP-2000; 2000US-236111P.
29-SEP-2000; 2000US-236842P.
29-SEP-2000; 2000US-236842P.
29-SEP-2000; 2000US-236842P.
20-CT-2000; 2000US-236891P.
02-CT-2000; 2000US-237178P.
02-CT-2000; 2000US-23713P.
03-CT-2000; 2000US-237316P.
03-CT-2000; 2000US-237316P.
03-CT-2000; 2000US-237316P.
03-CT-2000; 2000US-237369P.
03-CT-2000; 2000US-237360P.
03-CT-2000; 2000US-237604P.
03-CT-2000; 2000US-237604P.
03-CT-2000; 2000US-237604P.
01-NOV-2000; 2000US-237606P.
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ACCTGCGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGGAGGAGGCCC
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05-JUN-2000; 2000US-209473P

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The present invention describes a method (M1) for screening for an action action action describes a method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in capression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABLG1664 comprises a sequence (S) selected from 8447 sequences (given in ABLG1664 comprises in sequence (S) selected from 8447 sequences (given in ABLG1664 comprises in action or is at least 95% identical to (S), where a change in cappression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in que therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producin a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the creatment of cancer such as colon, breast, stomach, lung, thyroid, adenocarcinoma, varian, xidney, prostate or pancreatic cancer, adenocarcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, squamous cell carcinoma, neuroendocrine infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
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2000US-236033P.
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Weaver Z;
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             55.2%; Score 589.4; DB 24; Length 3088; llarity 78.7%; Pred. No. 1.2e-154; Conservative 0; Mismatches 191; Indels 0;
723 A; 839 C; 798 G; 728 T; 0 other;
BP;
                    Similarity
Seguence 3088
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136 GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes pig H transferase used in an example of the present invention. The present invention describes nucleic acids (NA) encoding a chimaric glycosyltransferase. The NAs comprise a catalytic domain of a first glycosyltransferase (GT) and a localisation signal of a second GT, whereby when the NA is expressed in a cell and where the chimaric enzyme is located in an area of the cell where it is able to compete for substrate with a second GT, resulting in reduced levels of a product from the second GT. The NAs can be used to produce cells and organs with desired glycosylation patterns. Products and methods of the epitopes in cells, tissues or organs which may be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 ATCCCATGGCAGAATIACCATCTCAACGACTGGAGGAGGGTTACCGCCACATTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCTTTGCACTGGCCASGATGAACGGACGGCTTGCGTTCATCCCCGCATCCATGCACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGGGACACGGCCAAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dene
                                                 transferase; chimeric; glycosyltransferase; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding chimeric glycosyltransferases - used for altering carbohydrate levels on the surface of cells, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 423.8; DB 19; Length 1098;
Pred. No. 1.9e-108;
0: Mismatches 252; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1098 BP; 181 A; 367 C; 312 G; 238 T; 0 other;
                                                                                                                                                                                                                                                                 transferase"
                                                                                                                                                                                 Location/Qualifiers
1..1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  altering carbohydrate levels on therapy and transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transplantation or gene therapy.
H transferase encoding cDNA
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69.68;
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/product= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sandrin MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           591; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AUST-) AUSTIN RES INST
                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-159170/14.
P-PSDB; AAW53102.
                                                                               transplantation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                               WO9805768-A1
                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                              12-FEB-1998
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Best Local S:
Matches 591
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AAV21640 standard; cDNA; 1098

RESULT 11

AAV21640

AAV21640 ID AAV2 XX AC AAV2

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                                                                                                                                                                                                                     834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Swine alpha(1,2) fucosyltransferase; FUT1; Escherichia coli, resistant; E. coli-associated intestinal disorder; E coli infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                     GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG
                    CCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAGGAGGCCCAGGCCTTC
                                                                           GIGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGTGAC
                                                                                                                                                                        GCCGCTTACCTCCAGCAGCTATGGACTGGTTCCGGGCCCGGATACGAAGCCCCCGTCTTT
                                                                                                                                                                                                                                                      CTGCGT-----GGTCTGCGGGTGAATGGGAGCCAGCCGAGTACTTTGTGGGGTGTCCAT
                                                                                                          GTGCGCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTGGAAGGGCGTGGTGGTGAC
                                                                                                                                                     CGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCTTC
                                                                                                                                                                                               GTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCCCGAGGAGAC
                                                                                                                                                                                                           CAGTGCAACCACCATCATGACTATTGGGACCTTTGGGATTTGGGCTGCCTACCTGGCA
                                                                                                                                                                                                                                                                                                                              GGTGGTGATACCATCTACTTAGCCAACTACACCTTCCGGATTCTCCGGTTCCTCAAAGTC
                                                                                                                                                                                                                                                                                                                                                                        TTTAAGCCAGAGGCAGCCTTCCTACCCGAATGGGTGGGCATCCCTGCCGATCTGTCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fragment of pHT83xF encoding swine alpha(1,2) fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
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9..1106
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                                                                                                                                                               The present sequence encodes swine alpha(1,2) fucosyltransferase (FUT1). The specification describes methods relating to Escherichia coli-resistant swine. One of the methods for identifying a swine resistant to E. coli-associated intestinal disorders, comprises determining whether the base at 307 of alpha(1,2) fucosyltransferasel gene (FUT1) is adenine (sic), in which case the swine are resistant. I porcine FUT1 polymorphisms can be used to develop drugs for the treatment of swine having E. coli-associated disease. The methods can also be used in preeding programmes to identify swine with resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                   543 GAGCAGATCCCCAGCGAGCTTCACCTGCACCACCTTCGGCAAGAGGCCCAGGGGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGGGGACACGGCCAAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCCGAGGTAGACAGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 ATCCCATGCCAGAATTACCATCTCAACGACTGGATGGAGGAGCGTTACCGCCACATTCCG
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                                                                         Identifying swine genetically resistant to E. coli associated diseases - using PCR-RFLP to assay for polymorphisms in the alpha(1,2) fucosyltransferase 1 gene
                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                       Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 252;
                                                                                                                                                                                                                                                                                                                                                                   Score 423.8; DB Pred. No. 2e-108;
                                                                                                                                                                                                                                                                                                                                                                                                  ·
0
                                                                                                                                    Claim 6; Fig 1; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                   39.78;
69.68;
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                              WPI; 1999-131692/11.
                                                                                                                                                                                                                                                                                                        to E coli infection.
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                            P-PSDB; AAW97356
Bosworth BT;
                                                                                                                                                                                                                                                                                                                                                                                  Best Local Sim
Matches 591;
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495 602 609 722 782 729

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and the assay itself is used as a basis for a kit, applied to swine of any age, in detecting polymorphisms associated with E. coli F18 receptors. The polymorphisms are useful in developing drugs to treat swine with E. coli-related diseases. However, a mutated form of the porchine FUTI gene may interfere with the normal enzyme and prevent it from producing the intestinal receptor for F18 The detection of polymorphic markers in the method disclosed enables the detection and treatment of E. coli-related intestinal diseases in swine, where there
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  483 GAGCCTGGCTGACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCGG
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                                                                                                                                                                                                                                                                                                                                 243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG
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                                                                                                                                                   has been no success using antibiotics due to unsuccessful prophylaxis
                                                                                                                                                                                                                                                                                                                                                                    CTCTTTGCACTGGCCAGGATGAACGGACGGCTTGCGTTCATCCCCGCATGCACAAC
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                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                          252; Indels
                                                                                                                                                                                     Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 other;
                                                                                                                                                                                                                          DB 20;
                                                                                                                                                                                                                        Score 423.8; DB Pred. No. 2e-108;
                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                      39.7%;
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GGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGGTTCCTCAAAGTC
                                                                                       GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATC
                                                                                                                           TITAAGCCAGAGGCAGCCTTCCTACCCGAATGGGTGGGCATCCCTGCCGATCTGTCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New method of identifying swine that are resistant to intestinal colonisation by Escherichia coli - comprises use of genetic polymorphic markers, used for breeding swine resistant to Escherichia coli-related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Swine; pig; alpha-1,2-fucosyltransferase 1; FUT1; resistance; Escherichia coli; infection; oedema; postweaning diarrhoea; intestinal disorder; polymorphism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Swine alpha-1,2-fucosyltransferase 1 encoding DNA.
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Escherichia
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GGCATGTTCACGATACCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Improving weight gain in swine using swine genetically resistant
Escherichia coli and feeding swine high levels of plant based protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.7%; Score 423.8; DB 21; Length 1269; llarity 69.6%; Pred. No. 2e-108; Conservative 0; Mismatches 252; Indels 6;
                                                                                                                                                                                                                                                                                                             /*tag= b
/note= "adenine is substituted for guanine
resistant pigs"
                                                                                                                                                                               Alpha-1-2 fucosyltransferase; FUT1; pig; polymorphism; Escherichia coli; resistance; ss.
                                                                                                                                                                                                                                                                      /*tag= a
/transl_except= (pos:726..728, aa:Ala)
replace(315,A)
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 other;
                                                                                                                                                      Pig alpha-1-2 fucosyltransferase FUT1 gene.
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                                                                             ВP
                                                                          AA294417 standard; DNA; 1269
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                                                                                                                              (first entry)
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1083 CTCCAGATG 1091
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Best Local Similarity
Matches 591; Conserv
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                                                                                                                              18-JUL-2000
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                                                                                                                                                                                                                        Sus scrofa
                                                                                                                                                                                                                                                                                                  variation
                                                                                                    AAZ94417;
                                                             AAZ94417
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243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 GAGCAGATCCGCAGCGAGTTCACCCTGCACCACCTTCGGCAAGAGCCCCAGGGGTA 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 730 GIGGIGIICGCGGGCAAIGGIAITGAGGGGICGCCAGCCAAGGACTICGCGCTGCTCACC 789
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                                                                                                                                                                                                 GTCCTGGCCCCCGTGTTCCGCATCACGCTGTCCTGGCGCCCGAGGTAGACAGGCAC
                                                                                                                                                                                                                                                               316 ATCCCATGGCAGAATTACCATCTCAACGACTGGATGGAGGAGCGTTACCGCCACATTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene; pig; swine; alpha (1,2) fucosyltransferase; FUT1; weight gain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUT1 CDNA
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842

606

Gaps

495

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Feeding swine genetically susceptible to F18 Escherichia coli colonization with a low plant protein based diet increases weight gain and lowers intestinal disease associated with E. coli infection
                                                                                                                                      (BIOT-) BIOTECHNOLOGY RES & DEV CORP (USDA ) US SEC OF AGRIC.
                                                                                                                                                           Bosworth B, Ridpath J,
F18; Escherichia coli;
                                                                                                                                                                        WPI; 2002-391652/42.
P-PSDB; AAB47995.
                                                                                                            18-SEP-1998;
                                                                                                                         20-MAY-1997;
                                                                                US6355859-B]
                                                                                              12-MAR-2002
             scrofa
                                                      mutation
              Sus
                          Key
```

97US-047181P 98US-0151592

В;

Wiseman

/\*tag= b /phenotype= "Confers resistance to F18 E.

Socation/Qualifiers

/\*tag= a /product= "FUT1"

This sequence represents the swine alpha (1,2) fucosyltransferase (FUT1) gene. A FUT1 gene in which there is a base other than adenine at position 307, may be used for improving weight gain in swine that are genetically susceptible to F18 Escherichia coli. The weight gain may be activated by feeding a diet of at least 40% animal based proteins. The feeding method is used to control F18 E. coli associated intestinal disease in swine. GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGGCGAATACGCCACA Gaps Score 423.8; DB 24; Length 1269; Pred. No. 2e-108; 0; Mismatches 252; Indels 6; Sequence 1269 BP; 219 A; 414 C; 361 G; 275 T; 0 other; Claim 1; Column 13-18; 9pp; English. 39.7%; 69.6%; 591; Conservative Query Match Best Local Similarity 136 Matches δŽ

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                                                  GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACACTATGCCACG 302
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completed: May 26, 2003, 12:08:26 Job time Search

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| Sequence 14, Appl<br>Sequence 17, Appl<br>Sequence 113, Appl<br>Sequence 113, Appl<br>Sequence 113, Appl<br>Sequence 113, Appl<br>Sequence 113, Appl<br>Sequence 159, Appl<br>Sequence 159, Appl<br>Sequence 159, Appl<br>Sequence 159, Appl<br>Sequence 28, Appl<br>Sequence 28, Appl<br>Sequence 28, Appl<br>Sequence 28, Appl<br>Sequence 19, Appl<br>Sequence 15, Appl<br>Sequence 15, Appl<br>Sequence 15, Appl<br>Sequence 15, Appl<br>Sequence 15, Appl<br>Sequence 11, Appl<br>Sequence 11, Appl |            | RAT GANGLIOSIDE<br>ANSFERASE AND USES  | Length 1068;<br>Indels 0; Gaps 0;                                | AGGAATTACCGATGACGACT 60  | CAGAGATGCGACGGGACAGCGAGACGCATGGG 120<br>      | GCGGCTGGGGAACCAGATG 180                 | AACGGCTTGCGTTCATCCCC 240                      |
|--|------------|--|--|--|---|---|---|
| US-09-298-886-14<br>US-09-298-886-17<br>US-09-298-886-16<br>US-08-997-080-113<br>US-08-997-862-113<br>US-09-224-542-113<br>US-09-224-542-113<br>US-09-226-426-113<br>US-08-997-862-1159<br>US-09-997-862-159<br>US-09-324-542-159<br>US-09-324-542-159<br>US-09-298-886-28<br>US-09-298-886-28<br>US-09-298-886-28<br>US-09-298-886-28<br>US-09-298-886-28<br>US-09-298-886-28<br>US-09-298-886-29<br>US-09-298-886-19<br>US-09-298-886-19<br>US-09-298-886-19<br>US-09-298-886-19                       | ALIGNMENTS | 198886<br>al.<br>CIDS AND PROTEINS OF A RAT GANG.<br>FIC ALPHA1-2 FUCOSYLTRANSFERASE<br>S/09/298,886   | ; Score 1068; DB 4;<br>; Pred. No. 2.2e-305;<br>0; Mismatches 0; | CTCCAGCAGCGAATAGIGAAGCTCCAACCCCTGTCAGAGAAAGGAATTACCGATGACGATTTIIIIIIIIII | CAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGACC<br> | AATGGAGAGCTGCGGGGCATGTTCACGATCCATTCCATT | GGCGAATACGCCACACTCTTTGCACTGGCCAGGATGAACGGACGG |
| <b>みみはここりもなここりもなるならみ</b>   |            | S/09298 s et al EIC ACI EDE ROFE ER: US/ 9-04-26 2.0   | 00.08<br>00.08<br>ve   | AGTG<br>NGTG   | AAAC<br>                                      | - B<br>B<br>B                           | CTC<br>                                       |
| 11 12 12 12 12 12 12 12 12 12 12 12 12 1   |            | ion US, Holmes Holmes NUCLEJ THEREE 1.029 NUMBEF: 1999 5: 29 Ver. 2.   | 100<br>/ 100<br>rvative  | SCGAATA<br>  | CTCGGG2<br>        <br>CTCGGG2                | SCTECGG                                 | GCCACA<br>                                    |
| พพนนนนนนนนนนนนนน<br>พ่อกับทั้งเขาที่พักทั้งพักษัพ  |            | 6-9 (6.22) (6.22) (6.22) (6.22) (6.22) (6.22) (6.22) (6.22) (6.22) (7.22)  | ilarity I<br>Conservati  | CCAGCAC<br>  | CAAATGTCC<br>                                 | TGGAGAC<br>        <br>TGGAGAC          | CGAATAC<br>                                   |
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| 80000000000000000000000000000000000000   |            | RESULT 1 US-09-298-886 Sequence 9, Patent No. GENERAL INF. TITLE OF II TITLE O | Query Ma<br>Best Loc<br>Matches                                  | QY   | oy<br>Db                                      | Qy<br>Db                                | o <sub>y</sub><br>Db                          |
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Patent No. 6329170

GENERAL INFORMATION:

APPLICANT: Exic H. Holmes et al.

TITLE OF INVENTION: WUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE ALE REFERANCE: 8511-02

CURRENT APPLICATION WHERE: US/09/298,886

CURRENT FILING DATE: 1999-04-26

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7

LENGTH: 1149
                                                                                                                                                                                           GGTGTCCATGTGCGCCCAGGGGACTATGTGCATGTCATGCCTAATGTGTGGAAGGGCGTG
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                 TACCACCACCTGCGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAG
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US-09-298-886-7
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TITLE OF INVENTION: GDP-L-FUCOSE: BETA-D-GALACTOSIDE
TITLE OF INVENTION: 2-ALPHA-L-FUCOSTITRANSFRASES,DNA SEQUENCES ENCODING THE
TITLE OF INVENTION: SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
TITLE OF INVENTION: GENOTYPING A PERSON
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                                                              ACTATTGGGACCTTTGGGATTTGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTA
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APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
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TELEPHONE: (703) 413-3000
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MOLECULE TYPE: DNA (genomic)
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TELEFAX: (703) 413-220
TELEX: 24885 OPAT INFORMATION FOR SEQ ID NO: 7:
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FILING DATE: 28-FEB-1995
CLASSIFICATION: 435
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nucleic acid
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MEDIUM TYPE: Floppy
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COUNTRY:
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APPLICANT: SANDRILON

TITLE OF INVENTION NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES

FILE REFERENCE: 30562.505W0

CURRENT APPLICATION NUMBER: US/09/254,077A

CURRENT FILING DATE: 1999-06-11

PRIOR PPLICATION NUMBER: PO 1823

PRIOR FILING DATE: 1996-08-22

PRIOR APPLICATION NUMBER: PO 1823

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PATENT VET. 2.1

SEQ ID NO 5.
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Length 1043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 612.8; DB 4;
Pred. No. 3.7e-171;
0; Mismatches 172;
                                                                                                             Sequence 5, Application US/09254077A Patent No. 6399758
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80.6%;
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Best Local Similarity 80.6
Matches 716; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Sus scrofa
                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               1043
                                                                                         US-09-254-077A-5
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C--GECTACCTGCAGCGGGCCCTGGACTGGTTCCGGGCCTGCTGCTGCCGCCTCCCGGTCTTT 779
                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                               ZIP: 22202
COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS:
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56..721
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FEATURE:
                                                                                                                                                                                                                                                                                                                    LOCATION:
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; LOCATION:
US-08-395-800A-1
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2-ALPHA-L-FUCOSYLTRANSFERASES, DNA SEQUENCES ENCODING THE
SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
GENOTYPING A PERSON
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                    TCGTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCCCGAGGAG
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                                                                                                                                                                                                     CCCAGIGCAACCACCAICAIGACIAIIGGGACCIIIGGGAIIIIGGGCIGCCIACCIGG
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                                                                                                                                             ACATTCCGGGACACTTTGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACC
                                                                                                                                                                                                                                     AGGCCTICCTGCGTGTCTGCGGGTGAATGGGAGCCAGCCGAGTACTTTTGTGGGTGTCC
                                                                                                                                                                                                                                                                                                                              ACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCT
                                                    TGCACACGGTGTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTACACACAGCGACACGG
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Patent No. 580732
GENERAL INFORMATION:
APPLICANT: LENNON, GREGORY
APPLICANT: LENNON, GREGORY
APPLICANT: CONGIL, DOMINIQUE
APPLICANT: KELLY, ROBERT J
TITLE OF INVENTION: 2-ALPHA-L-FUCOS:
TITLE OF INVENTION: SAME, METHOD FY
TITLE OF INVENTION: SAME, METHOD FY
TITLE OF INVENTION: GAME, METHOD FY
TITLE OF INVENTION: SAME, METHOD FY
TITLE OF INVENTION: GAME, METHOD FY
NUMBER OF SEQUENCES: 22
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US-08-395-800A-1
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130 CIGCGGGGCAIGITCACGAICAATICCATIGGCCGGCTGGGGAACCAGATGGGCGAAIAC 189
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ADDRESSEE: OBLON, SPIYAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITX: ARLINGTON STATE: VIRGINIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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PRIOR APPLICATION DATA: No. 5750176 applicable TELECOMMUNICATION INPORMATION: TELEPHONE: (614) 624-7080
TELEX: (514) 624-3074
TELEX: No. 5750176e
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SOFTWARE: WORDPerfect Version 6.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,889A
FILING DATE: 09-MAR-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Donald O. Nickey
ADDRESSEE: ROSS Products Division
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America 2IP: 43215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08208889A Patent No. 5750176 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           625 Cleveland Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1083 CTCCAGATG 1091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               970 CICCITAAG 978
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STREET: 62
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                                                                                                                                                           900 caerdecaaccacaccarcarcarcargagacaccrrcagagarcragagacacaraccrcaga 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 ATCCCATGGCAGAATTACCATCTCAACGACTGGATGGAGGAGCGTTACCGCCACATTCCG 375
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                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
BAPLICANT: Rideath, Julia
APPLICANT: Wiseman, Barry
TITLE OF INVENTION: INTERACTIONS BETWEEN GENOTYPE AND DIET IN SWINE THAT
TITLE OF INVENTION: PREVENT E. COLI ASSOCIATED INTESTINAL DISEASE
FILE REFERENCE: 21419-90119
CURRENT APPLICATION NUMBER: US/09/151,592
CURRENT APPLICATION NUMBER: 1999-09-18
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATENT OF VET. 2.0
                                                                              790 CAGTGCAACCACCATCATGACTATTGGGACCTTTGGGATTTGGGATGCCTACCTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCCAGCCTTCATCCAGCCTGCCATGCACGCC
GIGGTIACAAGCAACGGTAIGGCCIGGIGCCGGGAGAACAIIAATGCIICCCGAGGAGAC
                                                                                                                                                                                           GGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGGTTCCTCAAAGTC
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                 GGACACTTTGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACCACCTGCGC
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69.6%; Pred. No. 2.2e-115;
Live 0; Mismatches 252;
                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09151592
Patent No. 6355859
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ORGANISM: Swine
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US-09-151-592-1
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1023 TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAAAGGAGAGACTTGTCTCCA 1082
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543 GAGCAGATCCGCAGCGAGTTCACCCTGCACCACCTTCGGCAAGAGGCCCCAGGGGGTA
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                                                                                                                                                                                                                                                                                           610 CGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCTTC
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                                                                           CTGCGT-----GGTCTGCGGGTGAAIGGGAGCCAGCCGAGTACTTTGIGGGTGTCCAT
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TITLE OF INVENTION: Transgenic Production of Oligosaccharides NUMBER OF SEQUENCES: 1
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Cummings, R., Kopchick, J., Mukerji, P.,
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     512 GATCCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCCGG 571
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb:
COMPUTER: IBM Compatible
CPERATING SYSTEM: MS-DOS Version 6.21
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ADDRESSEE: ROSS Products Division
ADDRESSEE: Abbott Laboratories
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Abbott Laboratories
STREET: 625 Cleveland Avenue
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Patent No. 5891698
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APPLICATION NUMBER: US/08
FILING DATE: 02-MAY-1995
CLASSIFICATION:
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APPLICATION NUMBER: 08/2
FILING DATE: 09-MAR-1994
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                                                                            TOPOLOGY: Unknown
MOLECULE TYPE: Cloned cDNA representing the product of a
MOLECULE TYPE: human genomic DNA segment
DESCRIPTION: GDP-L-fucose - D-galactoside 2-alpha-fucosyl-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA
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                                                                                                                                                                                                                                                                                                                                                                Human Epidermal Carcinoma Cell line
                                                                                                                                                                              FRAGMENT TYPE: Entire amino acid sequence provided. ORIGINAL SOURCE: Human Epidermal Carcinoma Cell line
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Journal of Biological Chemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-208-889A-1
            SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Single
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INFORMATION FOR SEQ ID NO:
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DEVELOPMENTAL STAGE:
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CHROMOSOME/SEGMENT:
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   LIBRARY:
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TISSUE TYPE:
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                                                                                                                                                 HYPOTHETICAL:
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CELL LINE:
                                                                                                                                                                                                                 ORGANISM:
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Matches
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APPLICANT: Lowe, John B.

TITLE OF INVENTION: Method and Products For the Synthesis of
TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids,
TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned
TITLE OF INVENTION: Genetic Sequences That Determine These Structur
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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                                                                                  GGACACTTTGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACCACCTGCGC
                                                                                                      632 CIGGGTCAGCICCGCCTGGGCCGCACGACGGCACCTTTGTCGCGTCCAC
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P.C.
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00899
FILING DATE: 19910214
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ZIR: 22202
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ADDRESSEE:
STREET: 175
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PCT-US91-00899-10
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IDENTIFICATION METHOD: DNA sequencing and restriction analysis
IDENTIFICATION THE encoded product of nucleotide SEQ ID NO:
OTHER INFORMATION: 1: is the enzyme, GDP-L-fucose--D-galactoside 2-alpha-fucosy
OTHER INFORMATION: Which has the amino acid sequence described in SEQ. ID NO:1:.
OTHER INFORMATION: is responsible for the synthesis of 2'-fucosyllactose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 AICCCATGGCAGAATTACCATCTCAACGACTGGATGGAGGAGCGTTACCGCCACATCCG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451
                                                                                                                                                                                                            MOLECULE TYPE: Cloned cDNA representing the product of a MOLECULE TYPE: human genomic DNA segment DESCRIPTION: GDP-L-fucose- -D-galactoside 2-alpha-fucosyl-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCTTTGCACTGGCCAGGATGAACGGACGGCTTGCGTTCATCCCCGCATCCATGCACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Epidermal Carcinoma Cell line
                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: Entire amino acid sequence provided. ORIGINAL SOURCE: Human Epidermal Carcinoma Cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 408.2; DB 2;
Pred. No. 8.5e-111;
0; Mismatches 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Journal of Biological Chemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-433-271-1
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 624-7080
IELEFAX: (614) 624-3074
TELEX: No. 5891698
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: is responding to the AUTHORS: V.P. Rajan, et al. TILE: JOURNAL: JOURNAL: JOURNAL: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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ilarity 68.7%;
Conservative C
                                                                                                                                                                                    Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAGES: 11158 - 11167
                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE: HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                   Unknown
                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE:
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                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE TYPE:
CELL TYPE:
                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL LINE:
ORGANELLE:
                                                                                                                                                                                                 TOPOLOGY:
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Best Local Simi
Matches 579;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATE: 191
                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                     ANTI-SENSE
                                                                                                                                                                                                                                                                                                                                                        STRAIN:
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APPLICANT: FOUGUIER, SYLVIE
APPLICANT: GORGI, DOMINIQUE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: GELLY, ROBERT J
TITLE OF INVENTION: 2-ALPHA-L-FUCOSE: BETA-D-GALACTOSIDE
TITLE OF INVENTION: 2-ALPHA-L-FUCOSYLITRANSFERASES, DNA SEQUENCES ENCODING THE
TITLE OF INVENTION: GENOTYPING A PERSON
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
     799 CAGIGCAACCACCATTAIGACCATIGGCACCITCGGGCTICIGGGCIGCCIACCIGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 GGCATGITCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA 195
                                      GGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGGTTCCTCAAAGTC
                                                                                                           910 TITAAGCCAGAGGCAGCCTTCCTACCCGAATGGGTGGGCATCCCTGCCGATCTGTCCCA
                                                                                                                              859 GGCGGAGACTGTCTACCTGGCCAACTTCACCTGCCAGACTCTGAGTTCCTGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,800A
FILING DATE: 28-FEB-1995
CLASSIFICATION: 435
TELECOMMUNICATION: NFORMATION:
TELECHORE: (703) 413-220
TELERA. 248855 OPAT UR
INFORMATION FOR SEC ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 405; DB 1; L
Pred. No. 7.4e-110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08395800A
Patent No. 5807732
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LOWE, JOHN B
APPLICANT: LENNON, GREGORY
APPLICANT: ROUQUIER, SYLVIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.9%;
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Best Local Similarity 68.4 Matches 577; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
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39..1133
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OPERATING SYSTEM:
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                                                                                                                                                                                970 CTC 972
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                                                                                                                                                                                                                                                                                       US-08-395-800A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIGGTIACAAGCAACGGIAIGGCCIGGIGCCGGGAGAACATIAAIGCTTCCCGAGGAGAC 729
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 405; DB 5; Length 99
Pred. No. 7e-110;
0; Mismatches 260; Indels
              ATTORNEY/AGENT INFORMATION:
NAME: Lavallaye Ph.D., Uean-Paul
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-5940
TELEFAX: (703)466-2347
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 999 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                     37.9%;
                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        577; Conservative
                                                                                                                                                                                                                                S: unknown unknown
                                                                                                                                                                                                                                                                                                                                                   ; TISSUE TYPE: Blood
PCT-US91-00899-10
                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: HOM
                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
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Best Local S
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136 GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGCGACACGGCCAAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 37.9%; Score 405; DB 5; Le Best Local Similarity 68.4%; Pred. No. 7.5e-110; Matches 577; Conservative 0; Mismatches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE: expression of a human GDP-L-fucose: TITLE: D-galactoside 2-alpha-L-fucose: TITLE: Goosyltransferase DNA that can TITLE: form the H blood group antigen. JOURNAL: Proceedings of the National JOURNAL: Academy of Sciences, USA
          storage
                                                                                                                                                                                                                                                                                                                                                           ALX-144.1PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVILSENSE. NO PUBLICATION INFORMATION:
AUTHORS: Larsen, R.D. AUTHORS: Ernst, L.K. AUTHORS: Nair, R.P. AUTHORS: Lowe, J.B. TITLE: Molecular cloning, sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1174 Dase pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TCPOLOGY: Linear
NOLECOLE TYPE: CDNA to mRNA
DESCRIPTION: Human H-transferase
HYPOTHERICAL: No
                                                                                            APPLICATION NUMBER: PCT/US95/07554 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/278,282
FILING DATE: July 21, 1994
CLASSIFICATION:
  MEDIUM TYPE: 3.5 inch, 750 Kb. COMPUTER: Dell 486/50 OPERATING SYSTEM: DOS 6.2 SOFTWARE: WOYGPERFECT 6.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                08/260,201
                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Klee, Maurice M.
REGIENATION UNDRER: 30,399
REFERENCE/DOCKET NUMBER: ALX-
TELECOMMUNICATION INFORMATION:
TELEFRAN: (203) 255-1400
TELEFRAN: (203) 255-1400
TELEFRAN: (203) 255-1400
TELEFRAN: (203) 255-1101
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/260
FILING DATE: June 15, 1994
CLASSIFICATION:
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DATE: SEP-1990
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GENERAL INFORMATION:
APPLICANT: Sandrin, Mauro S.
APPLICANT: Podor, William L.
APPLICANT: Rother, Russell P.
APPLICANT: Squinto, Stephen P.
APPLICANT: McKenzie, Ian F. C.
TITLE OF INVENTION: Methods for Reducing
TITLE OF INVENTION: Myperacute Rejection of Xenografts
NUMBER OF SEOURNESS:
CORRESPONDENCE ADDRESS:
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STATE: Connecticut
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Pred. No. 7.6e-110;
0; Mismatches 260;
TELEFAX: (703) 413-3000
TELEFAX: (703) 413-220
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SEQUENCE CARACTERISTICS:
LENGTH: 1199 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Best Local Similarity
Matches 577; Conserv
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US-08-395-800A-5
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ROUGUIER, SYLVIE
ROUGUIER, SYLVIE
ROUGUIER, SYLVIE
KELLY, ROBERT J
WENTION: GD-1-FUCOSE: BETA-D-GALACTOSIDE
VENTION: 2-ALLPHA-L-FUCOSYLTRANSFERASES, DNA SEQUENCES ENCODING THE
VENTION: SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
VENTION: GENOTYPING A PERSON
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                     CCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAGGAGGCCCAGGCCTTC
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DAVIS HIGHWAY, SUITE 400
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IBM PC compatible
YSTEM: PC-DOS/MS-DOS
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US-08-395-800A-5
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                                                                                                                                                 APPLICANT: DIAMON, LISA E
APPLICANT: LOGAN, JOEN S
APPLICANT: BYRAE, GUERARD W
APPLICANT: SHARMA, AJAY
TITLE OF INVENTION: METHOD OF PRODUCING TRANSGENIC ANIMALS
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2268;
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/675,773B
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Pred. No. 1e-109;
                                                                                                                                                                                                                                                     .....KESSEB: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 SEVENTH STREET, N.W., SUITE 300
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIAMOND=1A
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03-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                        Sequence 4, Application US/08675773B Patent No. 6166288 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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; MOLECULE TYPE: DNA (genomic)
US-08-675-773B-4
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 68.4
Matches 577; Conservative
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                 1125 CTC 1127
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970 CTC 972
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1169 GIGCGCCGIGGGGACTATCTGCAGGTTATGCCTCAGGGCTGGAAGGGTGTGGTGGCGAC 1228 1469 GGGGGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGATC 1528 1529 TITAAGCCGGAGGCGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCCA 1588 670 GIGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCCCGAGGAGAC 729 730 GIGGIGITCGCGGGCAATGGIATIGAGGGTCGCCAGCCAAGGACTICGCGCTGCTCACC 550 GIGCGCCGAGGGGACTAIGTGCATGTCATGCCTAATGTGTGGAAGGGCGTGGTGGCTGAC 610 CGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCTTC 790 CAGIGCAACCACACCAICAIGACIAIIGGGACCIIIGGGAIIIGGGCIGCCIACCIGGCA 910 TTTAAGCCAGAGGCAGCCTICCTACCCGAATGGGTGGGCATCCCTGCCGATCTCTCCCCA 1409 CAGTGCAACCACCATTATGACCATTGGGCTTCTGGGCTGCTAGGGT 850 GGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGTTCCTCAAAGTC GENERAL INFORMATION:
APPLICANT: Falk, Per
APPLICANT: Falk, Per
APPLICANT: Gardon, Jeffrey I.
TITLE OF INVENTION: Animal Model for Gastro-Intestinal
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 E: Patrea L. Pabst 1100 Peachtree Street, Sequence 2, Application US/08273411 Patent No. 5625124 ATTORNEY/AGENT INFORMATION: NAME: Pabst, Patrea L. REGISTRATION NUMBER: 31,284 REFERENCE/DOCKET NUMBER: WU TELECOMMUNICATION INFORMATION: 496 CTGCGTGGTCTGCGGGTG CLASSIFICATION: 435 CITY: Atlanta STATE: Georgia COUNTRY: USA Georgia 1589 CTC 1591 970 CTC 972 FILING DATE:

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2412
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                                     1057
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        1058 GCCGGAGACACTGTCTACCTGGCCAACTTCACCTGCCAGACTCTGAAGATC
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                                                                                             GGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGTTCCTCAAAGTC
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APPLICATION NUMBER: 05/08/675,773B FILING DAIE: 03-JUL-1996 CLASSIFICATION: 800
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Pred. No. 1.3e-109;
0; Mismatches 260;
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: BYRNE, GUERARD W
APPLICANT: SHARNA, AJAX
TITLE OF INVENTION: FOR XENOT
NUMBER OF SEQUENCES: 42
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MOLECULE TYPE: DNA (genomic)
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NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,(
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Best Local Similarity 68.4'
Matches 577; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Patent No. 6166288
GENERAL INFORMATION:
APPLICANT: DIAMOND,
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TELEFAX: 2
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Pred. No. 1.2e-109;
0; Mismatches 260; Indels
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Proc. Nat'l Acad.
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 3373 base pairs
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68.48;
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OTHER INFORMATION: /not
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Search completed: May 26, 2003, 11:58:34 Job time : 60.2896 secs

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Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2003
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Run on:

May 26, 2003, 11:58:37 ; Search time 163.769 Seconds (without alignments) 8610.191 Million cell updates/sec

US-10-040-863-9 1068 Title: Perfect score:

1 ctccagcagcgaatagtgaa......gaagagccttctgatgggaa 1068 Seguence:

IDENTITY\_NUC Gapox 1.0 Scoring table:

828747 segs, 660231138 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Database :

Published\_Applications\_NA:\*

'Ggr2\_6'ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
'Ggr2\_6'ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
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'Ggr2\_6'ptodata/1/pubpna/US00\_PUBCOMB.seq:\*
'Ggr2\_6'ptodata/1/pubpna/US00\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description .  | ;               | Sequence 9, Appli | ņr            |                 | Sequence /, Appri | - K              |                    |                   | 4 m              | Ç.               | Sequence 12, Appl | - 2  | Sequence 5 appli | ,0               | , 0              | 7 0               |             |                  | 23,              |                  |
|-----------|----------------|-----------------|-------------------|---------------|-----------------|-------------------|------------------|--------------------|-------------------|------------------|------------------|-------------------|------|------------------|------------------|------------------|-------------------|-------------|------------------|------------------|------------------|
| SUMMARIES | ID             | TR-08-888-672-8 | US-10-040-863-9   | 229-666-60-SD | US-10-040-863-7 | US-09-051-034A-1  | US-09-954-456-45 | US-09-954-456-1621 | US-09-969-347-234 | US-09-051-034A-3 | US-09-844-268-12 | US-09-844-705-12  | ₹.   | US-09-863-475A-5 | US-09-999-672-29 | US-10-040-863-29 | TIS-09-908-672-23 | 00 00 00 00 | 05-09-999-672-26 | US-10-040-863-23 | US-10-040-863-26 |
|           | DB             |                 | 12                | 10            | 12              | 10                | 10               | 10                 | 10                | 10               | 10               | 10                | 6    | 10               | 10               | 12               | C                 | 1 -         | 7                | 12               | 12               |
|           | Length         | 1068            | 1068              | 1149          | 1149            | 1043              | 3088             | 3088               | 3088              | 1098             | 1269             | 1269              | 3373 | 8174             | 100              | 100              | 100               | o c         | 700              | 100              | 100              |
| о́Р       | Query<br>Match | 100.0           | 100.0             | 100.0         | 100.0           | 57.4              | 55.2             | 55.2               | 55.2              | 39.7             | 39.7             | 39.7              | 37.9 | 37.9             | 6.8              | 6.8              | 6.7               |             |                  | 6.7              | 6.7              |
|           | Score          | 1068            | 1068              | 1068          | 1068            | 612.8             | 589.4            | 589.4              | 589.4             | 423.8            | 423.8            | 423.8             | 405  | 405              | 72.8             | 72.8             | 71.2              | 71.0        | 7                | 7.1.             | 71.2             |
|           | Result         |                 | 7                 | ж             | 7               | 5                 | 9                | 7                  | 8                 | თ                | 10               | 11                | 12   | 13               | 14               | 15               | 16                | 17          | - C              | 18               | ნ 1              |

| 004747   | Sequence 98, Sequence 98, Sequence 16, Sequence 116, equence 113, equence 113,         |   | 241<br>78,<br>78,<br>19,                     |
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| 9-999-672-<br>0-040-863-<br>9-999-672-<br>9-999-672-<br>0-040-863- | S-10-125-540-9<br>US-09-764-870-<br>US-09-999-672-<br>US-10-040-863-<br>S-10-051-643-1 | 001-643-15 -880-505-15 -880-505-15 -040-863-2 -999-672-2 -040-863-2 -040-863-1 -040-863-1 | 9-880-10<br>-184-644<br>-184-634<br>-900-220 |
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## ALIGNMENTS

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61 CAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGACGGGACAGCGAGCAGCATGGG 120
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APPLICANT: Eric H. Holmes et al.
TILLE OF INVENTION: UNCLETC ACIDS AND PROTEINS OF A RAI CANGLIOSIDE
TITLE OF INVENTION: UNCLETC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT APPLICATION NUMBER: US/09/299,878
PRIOR APPLICATION NUMBER: US/09/298,886
PRIOR APPLICATION NUMBER: US/09/298,886
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100.0%; Score 1068;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1068; Conservative 0; Mismatches
                                   Sequence 9, Application US/09999672
Patent No. US20020127655A1
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Rattus norvegicus
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SOFTWARE: PatentIn Ver. 2.0
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LENGTH: 1068
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NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
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TYPE: DNA
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                                        ORGANISM: Rattus
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                         TACCGCCACATTCCGGGACACTTTGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTC
                                                                              CTGCTCACCCAGTGCAACCACACCATGACTATTGGGACCTTTGGGATTTGGGCTGCC
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                                            TACCACCACCTGCGCCCAGGAGTCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAG
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                                                                                                                  AATGGAGAGCTGCGGGCCATGTTCACGATCCAATTCCCATTGGCCGGCTGGGGGAACCAGATG
                                                                                                                                                                                             GCATCCATGCACAACGCTCTAGCGCCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGGC
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                    Indels
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Score 1068; I
Pred. No. 0;
; Mismatches
                   0;
100.0%;
Query Match 100.
Best Local Similarity 100.
Matches 1068; Conservative
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Sequence 9, Application US/10040863
Patent No. US20020137165A1
GENERAL INFORMATION:
APPLICANT: Eric H Holmes et al.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/10/040,863

US-10-040-863-9

CURRENT FILING DATE: 2001-11-01 PRIOR APPLICATION NUMBER: 09/298,886

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GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
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                                                                                                                                                                                                                                                                                AAE16622 standard; Protein; 380
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N-PSDB; AAD27207.
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cell transformation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is useful for inducing an immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
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                                                                                                                                                                                                                     Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNOM
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301 LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFELKAKGVTCYVAGRAF 353
                                                                                                                                                                                         Rat hepatoma H35 cell alphal-2fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PACI-) PACIFIC NORTHWEST CANCER FOUND.
                                                                                  AAB36104 standard; Protein; 380
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Best Local Similarity 100.
Matches 353; Conservative
                                                                                                                                                                                                                                                                            small cell lung carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sherwood AL;
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The invention relates to rat GM1-specific alphal-2fucosyltransferase (alphal-2FucT) enzyme and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate moiety found in ganglioside GM1, a terminal galactose betal-378-acetylgalactosamine (Galbetal-3GalNAc) saccharide. Alphal-2FucT DNA is useful for producing rat alphal-2FucT protein by recombinant techniques. Alphal-2FucT DNA is useful for the preparative synthesis of fucosyl containing glycolipids, glycoproteins, glycolipoproteins and oligosaccharide, and for preparing fucosyl GM1.
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                                                                                                                          300
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RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                                                                                                                                                                        LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 353
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/note= "Intracellular/Transmembrane domain"
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                                                          Modified-site
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                         W09807837-A1
                                                                                                                                   Modified-site
                                                                                                                                                                                  Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                             glycosyltransferase; FUT2; pig; epitope; antige
c animal; xenotransplantation; organ transplant.
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279..2
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251..2
                                                                                                                                                        /note= "transmembrane 27..340
                                                                                                                                 /note= "C~terminal domain"
185..187
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                                                                                                                                                                                           /note= "N-terminal cytoplasmic tail"
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                                            N-glycosylated
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SE or FUT2), a type II integral membrane profession affinity of type I and type III substrates. Its amino acid sequence was deduced from the nucleotide sequence of a genomic DNA clone (see AAV2903) isolated from a pig liver library on the basis of homology to human FUT2 cDNA. Pig FUT2 shows 83.2% identity with human FUT2. Expression of a glycosyltransferase, such as porcine Se, in a tissue results in reduced expression of unwanted carbohydrate epitopes on the tissue, especially porcine heart, liver, kidney or pancreas, rendering it more suitable for transplantation, i.e. less immunogenic and of increased immunological acceptability. A claimed method of producing a cell from a donor species that is immunologically acceptable to a recipient species involves reducing levels of carbohydrate on the donor cell that causes it to be recognised as non-self by the recipient by expressing a nucleic acid for a glycosyltransferase such as porcine Se in the cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding glycosyltransferase able to compete we second such enzyme - particularly used to reduce expression unwanted carbohydrate epitope(s) on tissues intended for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This polypeptide comprises porcine secretor glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Fig 1A-B; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-169148/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McKenzie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-AUG-1997;
 314
                                301
                                                                                                                                                                                                          134
                                                                                                                                                                         181
                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                            74
                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                               28
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            1 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                  LKVFKPEAAFLPEWVGIPADLSPLLK
                                                                                        RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                 GVHVRRGDYVHVMPNVWKGVVADRRYLEQALDWFRARYRSPVFVVSSNGMAWCRENINAS
                                                                                                                                                           GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                    YRHIPGEYVRLTGYPCSWTFYHHLRTEILREFTLHNHVREEAQDFLRGLRVNGSRPSTYV
                                                                                                                                                                                                                                                                                         GEYATLFALARNINGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
LKLFKPEAAFLPEWIGIEADLSPLLK
                                                                  RGDVVFAGNGIEGSPAKDFALLTQCNHTVMTIGTFGIWAAYLAGGETIYLANYTLPDSPF
                                                                                                                                                                                                                                     YRHIPGHEVRETGYPCSWTFYHHLRPEILKEETLHDHVREEAQAELRGLRVNGSQPSTFV
                                                                                                                                                                                                                                                                         GEYATLYALARMNGRPAFIPPEMHSTLAPIFRITLPVLHASTARRIPWQNYHLNDWMEER
                                                                                                                                                                                                                                                                                                                                           LQQRMVKIQP--TWELQMVTQVT---TESP-----SSPQLKGMWTINAIGRLGNQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUSTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV29003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sandrin MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96AU-0001823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-AU00540.
                                                                                                                                                                                                                                                                                                                                                                                                                                75.4%;
81.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1430;
Pred. No. 1
                                326
                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 19;
1.2e-147;
nes 19;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with
on of
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                  313
                                                                                                                                                                                                        193
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                                                                                                                                                                                                                                                                         133
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                                                                                                                                   253
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(first entry)

08-JUL-1998

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GVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIJTS
                           AAW69332 standard; Protein; 343
                                                                                                                                                                                                                                                                                                                                                                                                                             Lennon G,
                                                                                                                                                                       FUT2; nonsecretor genotyping.
                                                                                                                                                                                                                                                                                   95US-039580C
                                                                                                                                                                                                                                                                                                              95US-0395800.
                                                                                                             Human Sec2 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Kelly RJ,
                                                                                                                                                                                                                                                                                                                                        GIORGI D.
KELLY R J.
LENNON G.
LOWE J B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-520127/44
                                                                                                                                                                                                                                                                                                                                                                                              ROUQUIER S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 258; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV58323
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                   28-FEB-1995;
                                                                                                                                                                                                                                                                                                               28-FEB-1995;
                                                                                  20-NOV-1998
                                                                                                                                                                                                                           US5807732-A.
                                                                                                                                                                                                                                                       15-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                             Ď,
                                                         AAW69332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                         (GIOR/)
                                                                                                                                                                                                                                                                                                                                                       (KELL/)
(LENN/)
(LOWE/)
                                                                                                                                                                                                                                                                                                                                                                                                 (ROUQ/)
                                                                                                                                                                                                                                                                                                                                                                                                                             Giorgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197
  RESULT 7
              AAW69332
                                          δă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \Omega Y
                                                                                                                                                                                                                                                                                                                                                                                                                   present invention. The present invention describes nucleic acids (NA) domain of a first glycosyltransferase. The NAs comprise a catalytic a second Gr, whereby when the NA is expressed in a localisation signal of a second Gr, whereby when the NA is expressed in a cell and where the compete for substrate with a second Gr, resulting in reduced levels of a product from the second Gr. The NAS can be used to produce cells and organs with desired glycosylation patterns. Products and methods of the epitopes in cells, tissues or organs which may be used to reduce the levels of transplantation or gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                           example of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding chimeric glycosyltransferases - used for altering carbohydrate levels on the surface of cells, useful in gene therapy and transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 LOQRMVKIQP--TWELOMVTQVT---TESP-----SSPQLKGWWIINAIGRLGNQM 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YRHIPGHFVRFTGYPCSWTFYHHLRPBILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 340;
                        Pig; secretor; chimeric; glycosyltransferase; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents pig secretor used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.4%; Score 1430; DB 19;
81.9%; Pred. No. 1.2e-147;
iive 26; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                                                                                                                                                                                                                                                                                           Example 2; Fig 6; 51pp; English.
                                                                                                                                                                            96US-0024279.
                                                                                                                                                    97WO-AU00492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267; Conservative
                                                                                                                                                                                                                        (AUST-) AUSTIN RES INST.
                                                                                                                                                                                                                                                                             WPI; 1998-159170/14.
N-PSDB; AAV21639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 AA;
                                         transplantation
                                                                                                                                                                                                                                                   McKenzie IFC,
secretor
                                                                                            W09805768-A1
                                                                                                                                                  01-AUG-1997;
                                                                                                                                                                            21-AUG-1996;
02-AUG-1996;
                                                                                                                        12-FEB-1998
                                                                   Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
Pig
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Ωp δy q ŏ g g φ D,

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2;
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                                                                                                                                                                                                                                                                               Sec2; alpha(1,2) fucosyltransferase; H blood group; secretor genotyping; GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVYTSNGMAWCRENINAS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60

    useful for producing
    as secretor or nonsecretor

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YRHIPGHFVRFTGYPCSWTFYHHLRPBILKEFTLHDHVRBEAQAFLRGLRVNGSQPSTFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.1%; Score 1386.5; DB 19; Length 343; 79.1%; Pred. No. 7.3e-143; ive 26; Mismatches 31; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rouquier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lowe JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant enzyme and genotyping person
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Column 45-50; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding fucosyltransferase enzyme
AA.
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us-10-040-863-10.rag

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137 YRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRGLQVNGSRPGTF 196
                                                                                                                                    VGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The amino acid sequence codes for a protein capable of functioning as a GDP- Fuc:|Deta-D-Gal alpha(1,2)- fuocsyltransferase. The functional protein is represented by amino acids 33 to 365. The enzyme produced by the DNA sequence can be used in enzymatic (grosyltation of chain-terminating galactose residues on lactosemence or neolacto type beta-D-galactoside to alpha-2-L-fucose residues. See also ARR13749-R13752.
                                                                                                                                                       YRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTF
                                                                                                                                                                                                                SRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolation of gene conveying post-translational characteristic e.g. the presence of soluble or membrane bound oligo or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.5%, Score 1051.5; DB 12; Lengt
63.3%; Pred. No. 4e-106;
Live 37; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polysaccharide or glycosyltransferase.
                                                                                                                                                                                                                                                                                                                  FLKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                     AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 3; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ··
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR13751 standard; Protein; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90US-0627621.
90US-0479858.
90US-0480133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91WO-US00899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1991-267151/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 195; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR13751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIND ( IMND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-FEB-1990;
14-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9112340-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR13751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lowe JB;
                                                                                                                                                                                                                240
                  11
                                                                                                                                  180
                                                                                                                                                                         197
                                                                                                                                                                                                                                                   257
                                                                                                                                                                                                                                                                                          300
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                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                          AAR1375.
                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                            q
                                                                                                                                  δ
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                                                                                                                                                                                                                                                                                                                               pp
                                                       δ
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M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is given in a specification relating to a rat ganglioside GM_1-specific alphal-2fucosyltransferase protein. The protein or large callular fraction is useful for synthesis of a molecule comprising Fucalphal-2dalbetal-3GalNaA. a glycollipid, glycoprotein, glycolliportein or a free oligosaccharide comprising Fucalphal-2Galbetal-3GalNaC. The method involves contacting alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolpid, glycoprotein, glycolipoprotein or oligosaccharide having a terminal Galbetal-3GalNAC group. It is also useful for synthesis of fucosyl-GM_1 by contacting the protein with GDP-fucose and ganglioside GM_1. The obtained glycoproteins, glycolipids and oligosaccharides are useful as nutritional compositions and fucosyl-GM_1 is useful for inducing an immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                              neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAC; immunotherapy; immunosuppression; cancer; neurological disease; small cell lung carcinoma.
                                      257 HGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSPF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEVATLFALARMNGRLAFIPASMHNALAPIFRISLFVLHSDTAKKIPWQNYHLNDWMEER 120
                    241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGIFGIWAAYLAGGDTIYLANYTLPDSPF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOORIVKLOPLSEKELPMTTOMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNOM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 VQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGMWTINAIGRLGNQM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.6%; Score 1376; DB 2
78.9%; Pred. No. 1e-141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PACI-) PACIFIC NORTHWEST CANCER FOUND.
                                                                                                                    LKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                                                                                                                                               AAB36106 standard; Protein; 344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example, Fig 3B; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                 Human Sec2 catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US07384
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                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sherwood AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-687262/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200064464-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                       AAB35106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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Length 365;

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09-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                         AAR70422;
            Sequence
                                  Query Match
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                                                                                                                                                                                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                                                                                                                                                          odp-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase (Fuc-T) is encoded by cDNA (AAO98461) isolated from a human epidermal carcinoma cell line. The enzyme is responsible for the synthesis of 2'-fucosyllactose, one of the oligosaccharides in human milk. Other products of Fuc-T include glycoprotiens contg. beta-linked terminal galactose residues which can be fucosylated by Fuc-T. This DNA can be used to produce non-human transgenic mammals able to produce secondary gene products, e.g. oligosaccharides, in their milk. The transgenic mammals milk blochemically resembles human milk. This humanised milk can be used in the prepn. of an enteral nutritional product useful in the nutritive maintenance of an animal.
                                                                                                                262
                                                                                                                                        297
                                                                                                                                                              IQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 322
                                                                                                                                                                                    298 TQCNHTIMTIGTFGFWAAYLAGGDTVYLANFTLPDSEFLKIFKPEAAFLPEWVGINADLS 357
GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
                                    RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
                                                                                                                                                                                                                                                                                                                                                                                    GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase; Fuc-T; synthesis; 2'-fucosyllactose; oligosaccharide; human milk; non-human transgenic mammal; secondary gene product.
                                                                                Prodn. of human:ised milk by non-human transgenic mammal - by inserting heterologous gene encoding human catalytic entity which produces oligo:saccharide(s) and glyco:conjugate(s) into mammal's
                       NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL
                                                                                                                DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
                                                                                                                            GDP-L-fucose-beta-D-galactosidase alpha-1,2-fucosyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J, Moreman KW, Mukerji
Smith DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 62-64; 83pp; English.
                                                                                                                                                                                                                                                                                           AAR80154 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-US00926
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                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prieto PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-336739/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                           PLLKALTP 330
                                                                                                                                                                                                                                 358 PLWTLAKP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ98461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                      RESULT 10
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59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
                                                                                                                                                                                                                                                                                                                                           RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDXVHVMPNVWKGVVA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMBERYRHIPGHFVRFTGYPCSWTFYHHL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saps
                                                                                                                                                                                84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase; glycosyltransferase; glycosylation; oligosaccharide; glycoprotein; glycolipid; transgenic animal; cattle; milk.
                                                                                                                                                                                25 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2-Alpha-fucosyltransferase (AAR70422) is encoded by a cDNA clone (AAR01083) isolated from a human epidermal carcinoma A431 library. The enzyme can be expressed in this of a transgenic mammal the enzyme cow. This allows large-scale prodn. of oligosaccharides and
                                                         Length 365;
                                                                                                                   'n
                                                      Query Match
55.5%; Score 1051.5; DB 16; Lengt.
Best Local Similarity 63.3%; Pred. No. 4e-106;
Matches 195; Conservative 37; Mismatches 73; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kopchik JJ, Moremen KW, Prieto PA, Smith DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 62-64; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR70422 standard; Protein; 365 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2-Alpha-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-328284/42.
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365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 PLLKALTP 330
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Example 1; Page 45-47; 69pp; English
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15-JUN-1994;
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                                           Sequence
                                                           Query Match
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AAR90572
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                                                                                                                                                                                  TOCNHILMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 322
                                                                                                      NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFIGYPCSWTFYHHL 144
                                                                                                                                       RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alpha-1,2-fucosyltransferase (AAR70421) is encoded by a cDNA clone
                                                                    GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH
                                                                              DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in
                                                                                                                                                                                                                                                                                                                                                                            GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase; glycosyltransferase; oligosaccharide; glycoprotein; glycolipid; transgenic animal; cattle; glycosylation; milk.
                                  DB 16; Length 365;
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                                                   73; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catalyst - ure for produred in the milk,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mukerji
                                 55.5%; Score 1051.5; DB 63.3%; Pred. No. 4e-106; live 37; Mismatches 7
glycosylated proteins and lipids in the milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic animal expressing heterologous metabolite prodn esp. glycosyltransferase oligosaccharide(s) and glyco-conjugate(s) foods, pharmaceuticals, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kopchik JJ, Moremen KW, rieto PA, Smith DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 62-64; 84pp; English.
                                                                                                                                                                                                                                                                                                          AAR70421 standard; Protein; 365 AA.
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                                                                                                                                                                                                                                                                                                                                                            2-Alpha-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                           Best Local Similarity 63.3 Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prieto PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-328279/42.
N-PSDB; AAT01082.
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                                                                                                                                                                                                                                                             PLWTLAKP 365
                  365 AA
                                                                                                                                                                                                                                             PLLKALTP 330
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                WO9524488-A1
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                                                                                                                                                                                                                                                                                                                         AAR70421;
                  Sequence
                                  Query Match
                                                                                                                                                                                                                                                                                        RESULT 12
AAR70421
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263 TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWIFYHHL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 AALAPVFRITLPVLAPEVDSRTPWRELQLHDWMSEEYADLRDPFLKLSGFPCSWTFFHHL 177
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                               25 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 84
(AAT01082) isolated from a human epidermal carcinoma cell line A431 cDNA library. The enzyme can be expressed in the milk of a Lransgenic mammal, esp. cow. This allows large-scale prodn. of oligosaccharides or glycosylated proteins and lipids in the milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
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by introducing a vector expressing fucosyl:transferase into the
cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H-transferase; xenograft hyperacute rejection; transplantation; glycosyltransferase; galactose alpha(1,3) galactose.
                                                                                                                                                                                        Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Squinto
                                                                                                                                                                                        DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rother RP, Sandrin MS;
                                                                                                                                                                                      55.5%; Score 1051.5; DB 16 63.3%; Pred. No. 4e-106; live 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR90572 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-US07554
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94US-0260201
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                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                  Best Local Similarity
Matches 195; Conserv
                                                                                                                                     365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 PLWTLAKP, 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 PLIKALTP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT12238
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DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The human H-transferase (AAR80572) product of a cDNA clone (AAT12238) prepd. from human epidermoid carcinoma cells (ATCC CRL 155 A-431) can be expressed in xenogeneic organs, tissues and cells using a vector such as papex-1 (AAT1239). This results in decreased expression of the non-human antigen galactose alpha(1.3) galactose on the surface of the organs etc. so that hyperacute rejection is reduced upon transplantation to humans.
                                                                                                                                                                                                                                        59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGREGNOMGQYATLLALAQINGRRAFILPAMH 117
                                                                                                                                                                                                                                                                                                         RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
                                                                                                                                                                                                                                                                                     NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 144
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                        25 GNTESPEMREDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase; alpha 1,2 FT; transgene; transgenic mouse; animal model; intestinal adhesion; Helicobacter pylori infection; stomach; small intestine; gut; epithelial cell; surface receptor; carbohydrate antigen; gastritis; peptic ulcer; neoplasia; gastric adenocarcinoma; Lewis antigen; fucosylation.
                                                                                                                                                                                                                                                                                                                                                                    ; Score 1051.5; DB 17; Length 365; pred. No. 4e-106; 37; Mismatches 73; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human alpha 1,2 fucosyltransferase (EC 2.4.1.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW23805 standard; Protein; 365 AA.
                                                                                                                                                                Ouery Match 55.5%;
Best Local Similarity 63.3%;
Matches 195; Conservative 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-0273411
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                                                                                                                                     365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 PLWILAKP 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-1994;
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                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.5%; Score 1051.5; DB 18; Length 365; 63.3%; Pred. No. 4e-106; tive 37; Mismatches 73; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alpha(1,2)-fucosyltransferase; glycosylation; oligosaccharide;
                    Animal model for Helicobacter pylori infection - comprising transgenic mouse expressing human enzyme promoting intestinal
                                                                                                                                                                                       transgenic mouse expresses, in its intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253
                                                                                                                                  Example 1; Columns 13-16; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human alpha(1,2)-fucosyltransferase
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Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 AA;
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                                                                               adhesion
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AAW13640
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Egault DJ, Lowe JB;
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WPI; 1997-192897/17.
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WPI; 1997-192897/17.
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New recombinant fucosyltransferase proteins - useful for modifying cell surface oligosaccharide structures
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KAM13640) is an enzyme involved in the expression of type I and II clood group H structures. Its amino acid sequence was deduced
CC (AAM13640) is an enzyme involved in the expression of type I and II clood group H structures. Its amino acid sequence was deduced
CC Expression of the fucosyltransferase animal cell lines provides
CC specific capabilities with respect to post-translational
modification of the oligosaccharides of expressed proteins or
CC lucosylation of chain-terminating galactose residues on
lactoseamine or neolacto type beta-D-galactose to alpha-2-
CC dicose residues. The enzyme can also be used to raise antibodies
CC as diagnostic reagents and to screen cpds. for fucosyltransferase
CC inhibitor activity.
XX
Sequence 365 AA;
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Y 323 PLLKALTP 330 | | | | | | 358 PLWTLAKP 365

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Search completed: May 27, 2003, 15:06:16 Job time: 45.7707 secs

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RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 300
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US-09-298-886-10
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Sequence 1, Appli
Sequence 6, Appli
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                                                                                                     May 27, 2003, 15:03:22 ; Search time 14.5136 Seconds (without alignments) 715.625 Million cell updates/sec
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Sequence 2, A
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Sequence 6, 7
Sequence 6, 7
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Sequence 8, 2
Sequence 8, 2
Sequence 11,
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
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Compugen Ltd.
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US-08-393-246-6
US-08-273-411-1
US-08-255-058A-6
US-08-395-800A-10
US-08-696-731-6
US-09-042-531-6
US-09-254-077A-11
PCT-US91-00899-12
US-09-254-077A-10
US-09-254-077A-10
US-08-395-800A-2
US-08-395-800A-3
US-08-395-800A-3
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US-09-254-077A-6
US-09-254-077A-7
US-09-254-077A-8
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US-09-254-077A-19
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US-08-208-837A-33
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Sequence 10, Application US/09298886
Sequence 10, Application US/09298886
Sequence 10, Application US/09298886
SEMERAL INFORMATION:
APPLICANT: Eric H. Holmes et al.
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: GMI-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES TITLE OF INVENTION: THEREOF FILE REPERENCE: 8511-029
CURRENT APPLICATION UMBER: US/09/298,886
CURRENT FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                             Sequence 3, P
Sequence 4, P
Sequence 6, P
Sequence 6, B
Sequence 3, P
Sequence 3, P
Sequence 4, P
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US-08-539-005-33
US-09-280-598-35
US-07-906-349A-6
US-08-220-151-22
US-08-413-118-22
US-08-413-446-22
S470718-3 446-22
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US-08-208-897A-6
US-08-539-005-6
US-08-539-005-6
US-08-815-176-3
US-08-815-176-4
US-08-815-176-4
US-09-311-743-6
US-09-311-743-6
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US-09-311-743-6
US-09-197-344-3
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ORGANISM: Rattus norvegicus
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Patent No. 6329170
EALERAL INDORMATION:
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAI GANGLICSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUGOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REPERBENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT FILING DATE: 1999-04-26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SANDRIN, MAURO S.
APPLICANT: MCKENZIE, IAN C. F.
APPLICANT: MCKENZIE, IAN C. F.
TITLE OP INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.505W0
CURRENT APPLICATION NUMBER: 105/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR PLICATION NUMBER: PCT/AU97/00540
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1996-08-23
PRIOR FILING DATE: 1996-08-23
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No. 1.1e-156;
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81.9%;
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; ORGANISM: Rattus norvegicus
US-09-298-886-8
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Best Local Similarity 100.
Matches 353; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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Best Local Similarity
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US-09-298-886-8
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APPLICANT: SANDRIN, MAURO S.
APPLICANT: MACENZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.50SWO
                                                                                                                                                                                                                                                                                                                  GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
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81.9%; Pred. No. 1.1e-156;
iive 26; Mismatches 19;
  Mismatches
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26;
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317 LKIFKPEAAFLPEWTGIAADLSPLLK 342
301 LKVFKPEAAFLPEWVGIPADLSPLLK 326
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; Patent No. 6329170
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 343
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US-09-254-077A-8
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Matches 258; Conserv
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                                                                                                                                                                                                                                             TITLE OF INVENTION: GPP-L-FUCOSE: BETA-D-GALACTOSIDE
TITLE OF INVENTION: 2-ALPHA-L-FUCOSILIRANSFERASES, DNA SEQUENCES ENCODING THE
TITLE OF INVENTION: 3AME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
TITLE OF INVENTION: GENOTYPING A PERSON
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                   STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 STATE: VIRGINIA
STATE: VIRGINIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/395,800A
FILING DATE: 28 FEB-1995
FILING DATE: A35
                           314 LKLFKPEAAFLPEWIGIEADLSPLLK 339
      301 LKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                                     Sequence 8, Application US/08395800A Patent No. 5807732
                                                                                                                                                                                   APPLICANT: LENNON, GREGORY
APPLICANT: SOQUIER: SYLVIE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 28-FEB-1995
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703) 413-3000
TELERAX: (703) 413-2220
TELES: 248855 OPAT UR
INFORMATION FOR SEC ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 amino acids
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Best Local Similarity 79.1%
Matches 258; Conservative
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                                                                                                     US-08-395-800A-8
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61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
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APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: UNCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHA1-2 FUCOSYLITRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
APPLICANT: SANDRIN, MAURO S.
APPLICANT: MCKENZIE, IAN C. F.
TITLE OF INVENTION NUCLEIC ACIDS FOR REDUCING CARBOHYDRAIE EPITOPES
FILE REFERENCE: 30562.50800
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: PCT/AU97/00540
PRIOR PLING DATE: 1997-06-22
PRIOR PLING DATE: 1996-08-23
PRIOR FILING DATE: 1966-08-23
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CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTUM OFF. 2.0
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LENGTE: 344
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51;
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                                                                                                 LKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                                 PCT-US91-00899-11; Sequence 11, Application PC/TUS9100899; GENERAL INFORMATION:
                                                                                                                                                                                            Sequence 12, Application US/09254077A Patent No. 6399758
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Matches 200; Conservative
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LENGTH: 373
TYPE: PRT
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                                                                                                                                                                          YRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTF 179
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APPLICANT: SANDRIN, MAURO S.
APPLICANT: MCKENZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRAIE EPITOPES
FILE REPRENCE: 30562.505W0
CURRENT APPLICATION NUMBER: US/09/254,077A
                                                                                                                                                                                                                                                                VGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINA
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                                                        DB 4; Length 344;
                                                    72.6%; Score 1376; DB 4; Length 3 78.9%; Pred. No. 2e-150; Live 26; Mismatches 31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/AU97/00540
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: PO 1823
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                      300 FLKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09254077A Patent No. 6399758
                                                              Best Local Similarity 78.9 Matches 258; Conservative
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Best Local Similarity 79.1
Matches 258; Conservative
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Lepus Sp. US-09-254-077A-9
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US-09-254-077A-9
                        US-09-298-886-11
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LENGTH: 347
                                                      Query Match
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APPLICANT: Lowe, John B.

TITLE OF INVENTION: Method and Products For the Synthesis of
TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids,
TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned
TITLE OF INVENTION: Genetic Sequences That Determine These Structur
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RGDVVFAGNGIEGSPAKDFALLTQCNHTIMIIGTFGIWAAYLAGGDTIYLANYTLPDSPF 300
                                        RGDVVFAGMGLESSPAKDFALLTQVNHTVWIIGTFGIWAAXLTGGDTIXLANYTLPDSPF 320
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APPLICANT: SANDRIN, MAURO S.
APPLICANT: MOKENZIE, IAN C. F.
TILLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.5500
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT APPLICATION NUMBER: US/09/2640
PRIOR APPLICATION NUMBER: PO 1823
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VET. 2.1
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US-08-393-246-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPEILKEFTLADHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 333;
                        ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                  SCFWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00899
FILING DATE: 19910214
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAVAILEY NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 1051.5; DB 5; Pred. No. 6.2e-113; 37; Mismatches 73;
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/07914281
Patent No. 5324663
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.5%;
                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703)521-5940
TELEFAX: (703)486-2347
TELES: 248855 OPAU UR
INFORMATION FOR SEQ ID NO: 13
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 333 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-terminal
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
             CORRESPONDENCE ADDRESS
NUMBER OF SEQUENCES:
                                                               CITY: Aringue.
STATE: Virginia
21P: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: pro
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: C-+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 PLLKALTP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326 PLWTLAKP 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-914-281-6
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OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE SIRUCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEXATLFALARMNGRLAFIPASMH 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 365;
        METHODS AND PRODUCTS FOR THE SYNTHESIS
                                                                                                                              1: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. P.C. 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                            SOFTMANE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/914,281
FILING DATE: 19920720
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye Jean-Paul M. P.
REGISTRATION UNDERSE: 31,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.5%; Score 1051.5; DB 1 63.3%; Pred. No. 7.2e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: LASTATION NUMBER: 31,451
REGISTRATION NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                    ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION: APPLICANT: LOWE, JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 365 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.3%
Matches 195; Conservative
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-07-914-281-6
TITLE OF INVENTION: M
TITLE OF INVENTION: G
TITLE OF INVENTION: G
TITLE OF SEQUENCES:
                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                 CITY: Arlington
                                                                                                                                                                                                                       Virginia
                                                                                                                                                                                                                                           U.S.A.
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6674-6678
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FRAGMENT TYPE:
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PAGES: bo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-273-411-1
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   METHODS AND PRODUCTS FOR THE SYNTHESIS OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GIYCOLIFIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 TQCNHTIMTIGIFGFWAAYLAGGDTVXLANFTLPDSEFLKIFKPEAAFLPEWVGINADLS 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                  E: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
E: P.C.
1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.5%; Score 1051.5; DB 1; 63.3%; Pred. No. 7.2e-113; tive 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: LAVALLEY, JEAN-Paul M. P.
REGISTRATION NUMBER: 31,451
TEFERENCE/DOCKET NUMBER: 2363-060-55
TEFENENCE/DOCKET NUMBER: 2363-060-55
                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 63.39
Matches 195; Conservative
                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SE
TITLE OF INVENTION: OF TITLE OF INVENTION: OF TITLE OF INVENTION: OF TITLE OF INVENTION: OF UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                     Arlington: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                  COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                      22202
                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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RESULT 13

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"GDP-L-fucose:beta-D-Galactoside-2-alpha-L-fucosyl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.5%; Score 1051.5; DB 1; Length 365; 63.3%; Pred. No. 7.2e-113; Live 37; Mismatches 73; Indels 3;
Sequence 1, Application US/08273411
Patent No. 562524
GENERAL INFORMATION:
APPLICANT: Falk, Per
APPLICANT: Gordon, Jeffrey I.
TITLE OF INVENTION: Animal Model for Gastro-Intestinal
WINDER OF INVENTION: Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: FROM 1 TO 365
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,411
                                                                                                                                                                      1: Patrea L. Pabst
1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                         STAIL.
COUNTRY: USA
ZIP: 30309-4530
ZOMPUTER READABLE FORM:
MEDIUM TYPER: Floppyy disk
~WEDIUM TYPER: IBM PC compatible
~VSTEM: PC COMPATIBLE
~VSTEM: PC DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: WILO
REFRENCE/DOCKET NUMBER: WILO
TELECOMMUNICATION INFORMATION:
TELEFAM: (404) 815-6508
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Larsen, et al.
Proc. Nat'l Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.3%
Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: 1..365 OTHER INFORMATION: /not PUBLICATION INFORMATION:
                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                      ADDALL
STREET: LICU
CITY: Atlanta
Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: Larsen,
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GDP-L-FUCOSE: BETA-D-GALACTOSIDE
2-ALPHA-L-FUCOSYLFRANSFERASES, DNA SEQUENCES ENCODING THE
SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
GENOTYPING A PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFÄGNGIEGSPAKDFALL 262
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                              298 IQCNHIINTIGIFGEWAAXLAGGDTVXLANFTLEDSEFLKIFKPEAAFLPEWVGINADLS 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT 1: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.5%; Score 1051.5; DB 1 63.3%; Pred. No. 7.2e-113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JMBER: US/08/395,800A
28-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                                                                               Sequence 6, Application US/08395800A Patent No. 5807732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                              APPLICANT: ROUQUIER, SYLVIE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (703) 413-3000
(703) 413-2220
                                                                                                                                                                                                                                                                                         APPLICANT: LOWE, JOHN B APPLICANT: LENNON, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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amino acid
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: G-A-TITLE OF INVENTION: 2-A-TITLE OF INVENTION: SAMITITLE OF INVENTION: GEWINDRER, OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE IYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 195; Conserva
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                                                                                                                                   358 PLWTLAKP 365
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COUNTRY:
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Sequence 6, Application US/08525058A
Patent No. 5770420
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
ATTILE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 AALAPVERITLEPVLAPEVDSRTPWRELQLHDWMSEEYADLRDPFLKLSGFPCSWTFFHHL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
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                                      IQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.5%; Score 1051.5; DB 1; 63.3%; Pred. No. 7.2e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2363-060-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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TELEPAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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; MOLECULE TYPE: protein
US-08-525-058A-6
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nes 195; Conserv
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STATE: Virginia
COUNTRY: U.S.A.
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STREET: 17
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US-08-525-058A-6
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                                                                                                                      May 27, 2003, 15:08:29 ; Search time 15.2516 Seconds (Without alignments) 2295.367 Million cell updates/sec
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1: /cggn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cggn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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5: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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2 US-10-040-863-10
2 US-10-040-863-8
2 US-10-040-863-8
3 US-09-051-034A-2
3 US-09-051-034A-2
3 US-09-051-034A-2
4 US-09-863-11
2 US-10-105-963-10
3 US-09-863-475A-6
3 US-09-844-268-13
4 US-09-844-268-13
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; Patent No. US200201371651
; GENERAL INFORMATION:
    APPLICANT: Exic H. Holmes et al.
    APPLICANT: Exic H. Holmes et al.
    TITLE OF INVENTION: UNIN-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
    TITLE OF INVENTION: HEREOF
    TITLE OF INVENTION: HEREOF
    TITLE OF INVENTION: UNIN-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
    TITLE OF INVENTION: HEREOF
    TITLE REFERENCE: 8511-029
    CURRENT APPLICATION NUMBER: US/10/040,863
    CURRENT FILING DATE: 1999-04-23
    NUMBER OF SEQ ID NOS: 29
    NUMBER OF SEQ ID NOS: 29
    SOFTWARE: PALENTIN Ver. 2.0
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TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GAL-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REPERBACE: 8511-029
CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT FILING DATE: 2001-10-31
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Patent No. US20020127655A1
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Matches 353; Conservative
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51 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEBR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                           241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 300
                                                                                                                                                                                                                                      61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                                                                                                        YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                             301 LKVFKPBAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 380;
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                                                                                                                Length 380;
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                                                                                                                  DB 10;
                                                                                                               Score 1896; DB 10;
Pred. No. 4.4e-188;
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                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION UNMBER: 09/298,886
PRIOR FILING DATE: 1999-04-23
NUMBER OF ARD ATTOMATION OF THE PRIOR FILING DATE: 1999-04-23
                                                                                                                    100.0%;
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Matches 353; Conservative
                                                                          norveqicus
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NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver.
                                                                                                                                    Similarity
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61 GEXATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                         GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                        APPLICANT: MCKERZIE, IAN FARQUIAR CAMPBELL
APPLICANT: SANDRIN, MAURO SERGIO
TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
TITLE OF INVENTION: GLYCOSYLIRANSFERASE
FILE REFERENCE: 30562.6USW0
CURRENT APPLICATION NUMBER: 0509/051,034A
CURRENT FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/024,279
PRIOR FILING DATE: 1996-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                     LKVPKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCXVAGRAF 353
                                                                                                                                                                    75.4%; Score 1430; DB 10; Length 340; 81.9%; Pred. No. 7.7e-140;
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                                                                                                                                                                                                                                                     Sequence 2, Application US/09051034A Patent No. US20010055584A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
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US-09-051-034A-2
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Best Local Similarity
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RESULT 6 US-09-999-672-11

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GENERAL INFORMATION:
APPLICANT: Eric H. Holmes et al.
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: GOCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GMA.-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT FILING DATE: 2001-10-31
PRIOR PELLING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE PREDENTION VOWER: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YRHI-PGHEVRFTGYPCSWTFYHHLRPEILKEFTLHDHVRBEAQAFLRGLRVNGSQPSTF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 VGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LQQRIVKLQPLSEKELPMTTQMSSGNIESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/10040863

Sequence 11, Application US/10040863

GENERAL INFORMATION:

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: MUCLEIC ACIDS AND PROTEINS OF A RAT GANGLICSIDE

TITLE OF INVENTION: GMI-SPECIFIC ALPHAl-2 FUCOSYLFRANSFERASE AND USES

FILE REFERENCE: 8511-029

CURRENT APPLICATION NUMBER: US/10/040,863

CURRENT PILING DATE: 2001-11.01

PRIOR FILING DATE: 1999-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.6%; Score 1376; DB 10; 78.9%; Pred. No. 3.1e-134; ative 26; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLKVFKPEAAFLPEWVGIPADLSPLLK 326
Sequence 11, Application US/09999672 Patent No. US20020127655A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.68;
78.98;
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SEQ ID NO 11
LENGTH: 344
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                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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US-10-040-863-11
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Best Local Similarity
Matches 258; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                     LENGTH: 344
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                SEQ ID NO 11
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APPLICANT: LOWE, JOHN B.

APPLICANT: LOWE, JOHN B.

TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS

OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,

GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION

OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMFNVWKGVVA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 DRGYLEKALƏMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 NALAPIFRISLPVLHSDTAKKIPWONYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 144
298 IQCNHTIMITIGIFGFWAAXLAGGDTVYLANFTLPDSEFLKIFKPEAAFLPEWVGINADLS 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 GNTESPEMREDSEQHGNGELRGMFTINSIGRLGNOMGEYATLFALARMNGRLAFIPASMH 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.5%; Score 1051,5; DB 10
llarity 63.3%; Pred. No. 1.5e-100;
Conservative 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPLICATION NUMBER: US/09/863,475A
PILING DATE: 24-May-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION NUMBER: 07/914,281
APPLICATION NUMBER: 07/914,281
ATTORNEY,AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 2363-060-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: US-09-863-475A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                             US/09863475A
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248855 OPAT UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22202
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
                                                                                                                                                                                                          Sequence 6, Application US, Patent No. US20020102688A1 GENERAL INFORMATION:
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Matches 195; Conserv
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                                                                                                          358 PLWTLAKP 365
                                                                    PLLKALTP
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Publication No. US20030068818A1
Sequence 10, Application US/10105963
Publication No. US20030068818A1
GENERAL INFORMATION:
GENO COFPORTION:
APPLICANT: Genon Corporation
APPLICANT: Clark, A. John
APPLICANT: Chark, A. John
APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: Aransplantation and a Carbohydrate Determinant Selection System
TITLE OF INVENTION: Recombination
FILE REPERENCE: 731/002
CURRENT APPLICATION NUMBER: US/10/105,963
CURRENT APPLICATION NUMBER: US 60/277,811
PRIOR FILING DATE: 2001-03-21
WINNER OF THING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
                                                                                                                                                                                                                 179
                                                                                                                                                                                                                                        61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                                                                                                                                                VGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINA 239
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              Gaps
                                                   LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
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                                                                                 121 YRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTF
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            31; Indels
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                 Mismatches
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                 26;
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SEQ ID NO 10
LENGTH: 365
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Best Local Similarity 63.3
Matches 195; Conservative
              Conservative
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                 258;
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TILE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY TILE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY TILE OF INVENTION: RESISTANT TO FIRE. COLI ASSOCIATED DISEASES; FILE REFERENCE: 21419/90368
CURRENT APPLICATION NUMBER: US/09/844,268
CURRENT FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 09/443,766
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENT OF SEQ ID NOS: 13
TENDAMER: PATENT OF SEQ ID NOS: 13
TENDAMER: PATENT OF SEQ ID NOS: 13
TENDAMER: PATENT OF SEQ ID NOS: 13
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TITLE OF INVENTION: METGODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
TITLE OF INVENTION: RESISTANT TO F18 E. COLI ASSOCIATED DISEASES
TITLE OF INVENTION: RESISTANT TO F18 E. COLI ASSOCIATED DISEASES
CURRENT APPLICATION NUMBER: US/09/844,705
CURRENT FILING DATE: 2001-04-27
PRIOR PILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 13
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62.6%; Pred. No. 8e-100;
Live 38; Mismatches 75; Indels
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Patent No. US200221386A1
GENERAL INFORMATION:
APPLICANT: BOSWORTH, BRAD
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 62.6%;
Matches 194; Conservative
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Matches 194; Conserv
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LENGTH: 365
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                                                                                                                              263 TQCNHTIMTIGFFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS
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APPLICANT: SANDRIN, MAURO SERGIO
TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS
FILE REFERENCE: 30562.6USW
CURRENT APPLICATION NUMBER: US/09/051,034A
CURRENT FILING DATE: 1998-03-31
PRIOR PILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/024,279
PRIOR PILING DATE: 1997-06-21
PRIOR PILING DATE: 1997-06-21
PRIOR PILING DATE: 1997-06-21
PRIOR PILING DATE: 1996-08-21
PRIOR PILING DATE: 1996-08-21
PRIOR PLING DATE: 1996-08-21
PRIOR PLING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 11
                                                         DB 10; Length 365;
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Matches 194; Conservative
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Sequence 14, Application US/09479614
; Sequence 14, Application Wo/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 1999-01-07
; EARLIER PFLICATION NUMBER: 60/115,033
; EARLIER PILING DATE: 1999-01-07
; SOFTWARE: Patentin Ver. 2.0
; SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                    APPLICANT: Yang, Yong Min APPLICANT: Yang, Yong Min APPLICANT: Barankiewicz, Theresa J. APPLICANT: Barankiewicz, Theresa J. APPLICANT: Chen, Zhong TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF FILLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF FILLE APPLICATION NUMBER: US/10/214,524 CURRENT PILLING DATE: 2002-08-08 PRIOR FILING DATE: 2001-08-13
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nilarity 25.0%; Pred. No. 0.14;
Conservative 21; Mismatches 84; Indels
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--ESHFEVKSQ 296
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                                                                                                                   Sequence 25, Application US/10214524 Publication No. US20030073142A1 GENERAL INFORMATION:
                                                                                                                                                                                          APPLICANT: Chen, Swey-Shen Alex
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SOFTWARE: Patentin version 3.1
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Matches 55; Conserv
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US-09-479-614-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 GIDYQKKALEYMAKRYPNMELFV-----FCE------DLKFTQNLDLGYPFTDMTTR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 ------LITQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPD----SPFLKVFK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 DKEEEAYWDMLLMQSCKHGIIANSTYSWWAAYL-----MEN---PEKIIIGPKHWLFG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 FILPPPPENNKNNKKEBEZQRKLS--LILAAKNSVF--VHIRRODYVGI-----GCOL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 FTL------HDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --LPVLHSDIAKKIPWQNYHLNDWMEERYRHI-PGHFVRFIGYPCSWTFYHHLRPEILKE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 QHLPKLVRDALKYIGFDRVSQBIVFEYEPKLIKPSRLTYFFGYFQDPRYFDAISSLÍKQT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TLFALARMNGRLAFIPASMHNALAPIFRIS-- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 GGLGNQMFQYAFAKSLQKHLNTPVLLDTTSFDWSNRKWQLELFPIDLFYANAKEIAIAKM 69
                                                                                                                                                                                                                                                                                                                                             PAKDFALLIQCNHTIMIIGTFGIWAAYLAGGDIIYLANYTLPDSPFLKVFKPEAAFLPEW 314
                                                                                                                                                                                                                                                                                                                                                                      254
            51 PVAIFCLAGTPVHPNASDSCPKH-PASFSGTWIIYPDGRFGNQMGQYATLLALAQLNGRQ 109
                                                                                        195 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS
                                                                                                                                                                                                                                                                             137 SWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMP
                                                             77 AFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09848838

Sequence 2, Application US/09848838

Patent NO. US20020037570A1

GENERAL INFORMATION:
APPLICANT: TAYLOr, Diane
APPLICANT: Palcic, Monica
APPLICANT: Palcic, Monica
APPLICANT: Palcic, Monica
FILE OF INVENTION: ALPHA 1, 2-FUCOSYLTRANSFERASE
FILE REFERENCE: 07254-061002
CURRENT FILING DATE: 2001-02-03

PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-04

PRIOR FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 23

SOSTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.4%; Score 141; DB 10;
24.0%; Pred. No. 2.9e-06;
tive 33; Mismatches 125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT; ORGANISM: Helicobacter pyloriUS-09-848-838-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 81; Conserv
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US-09-848-838-2
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186 RCDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGM--AMCRENINASRGD 243
229 -DLXVHKSPKI-TCLVVD------ 259
244 VVFAGNGIEGSPAKDFALLIQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSP---F 300
                                                                                   260 ----GESVHPDP---WVKKTQYNGTITVTSTLPVDATDWVEGET-YQCKVTHPDLPKDIV 311
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Search completed: May 27, 2003, 15:25:43 Job time : 16.2516 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

. May 27, 2003, 15:00:45 ; Search time 12.7916 Seconds (without alignments) 2652.940 Million cell updates/sec

Run on:

Title: Perfect score: Sequence:

US-10-040-863-10 1896 1 LOGRIVKLQPLSEKELPMTT.....RSHFHLKAKGVICYVAGRAF 353

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

.Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|    |               |   | a(1 2)finoceul | DT 3 - C - C - C - C - C - C - C - C - C - | 9474CCO374G | alantosido osa | יין היין כיין כיין כיין כיין כיין כיין כ | , מי<br>מי | במ" / | nrotein BOOGS 3 [4 | · ' |     |     | hypothetical prote | nypothetical prote | Ω,         | מ          | ical p |      |     | hypothetical proto |     |      | hyporhetical prote |     |     | ical              | hypothetical prote | ical | ר מיני | 3 6 | cal piot | ם מ | delization |
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|    | ä             | 9 :                                     | (1             | N  | 7           | N              | N  | 7          | C     | 7                  | ~   | (7  | 7   | 0                  | ۱ د                | 4 C        | 4 (        | 7 (    | 7    | ~   | N                  | N   | 3    | N                  | C   | 1   | 4 C               | ١,                 | ?    | ~      | C3  | 2        | ~   |            |
|    | Tength        |   | 343            | 354  | 373         | 365            | 159                                      | 142        | 281   | 443                | 363 | 348 | 335 | 383                | 500                | 000        | 100        | 300    | 00 i | 392 | 353                | 625 | 434  | 381                | 365 | 300 | ) (<br>) (<br>) ( | 7 1                | 1/7  | 317    | 355 | 348      | 597 |            |
| dР | Query         |   | 73.1           | œ.   | ~           | 'n.            | 4.                                       | ö          | H     |                    |     |     |     |                    |                    |            |            |        |      |     |                    |     |      |                    |     |     |                   |                    |      |        |     |          | 4.9 |            |
|    | Score         | , ,                                     | 1386.5         | 129  | ö           | 051.           |  | 28         |       | 18                 |     | 15  | 53. | 39.                | 38                 |            | - 7        |        |      |     |                    |     |      |                    | 17. | 1   |                   |                    | 7 (  | ò      |     | ω,       | 66  |            |
|    | Result<br>No. | 1                                       | Н              | 7  | m           | 4              | ın                                       | φ          | 7     | ω.                 | σ   | 10  | 11  | 12                 | 13                 | 14         |            | ) L    | 1 C  | 7 7 | 18                 | 19  | 20   | 21                 | 22  | 23  | 24                | 100                | 7 (  | 97     | 27  | 28       | 29  |            |

RESULT 2

| 1 92.5 4.9 398 2 T19293<br>2 92.5 4.9 776 2 B85384<br>4 9 776 2 B85384<br>8 9 4.7 353 2 JN0920<br>8 9 4.7 1334 2 B98348<br>8 9 4.7 1344 2 B98348<br>8 8 4.7 1344 2 B98348<br>8 8 4.7 2058 2 A59267<br>8 8 4.6 217 2 A50857<br>8 7 4.6 365 2 T45082<br>8 7 4.6 365 2 T45082<br>8 7 4.6 217 2 A43321<br>8 7 4.6 217 2 A43321   |
|--|
| 92.5<br>92.5<br>4.9<br>91.5<br>4.9<br>716<br>91.6<br>81.6<br>82.6<br>83.6<br>83.6<br>83.6<br>83.6<br>84.7<br>86.5<br>87.7<br>88.5<br>87.7<br>88.5<br>87.7<br>88.5<br>87.7<br>88.5<br>88.5<br>87.7<br>88.5<br>87.7<br>88.5<br>87.7<br>88.5<br>87.7<br>88.5<br>88.5<br>87.7<br>88.5<br>87.7<br>88.5<br>87.7<br>88.5<br>87.7<br>88.5<br>87.7<br>88.7<br>88.5<br>87.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88.7<br>88. |
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## ALIGNMENTS

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|--|---|--|---|--|---|--|--|--|
| change 21-Jul-2000<br>we, J.B.<br>Lman Secretor blood<br>.1; PID:9687619   | orotein   | Length 343;<br>Indels 11; Gaps   | PIINSIGRLGNOM 60<br>   :  :  :  :  :<br> TINAIGRLGNOM 76  | QNYHLNDWMEER 120<br>   | TERVNGSQPSTFV 180<br> -         <br> LOVNGSRPGTFV 196                     | GMAWCRENINAS 240<br>   | YLANYTLPDSPF 300<br>   |  |
| RESULT 1 A56099 alpha(1,2)fucosyltransferase Sec2, long form - human C;Species: Homo sapiens (man) C;Date: 03-Ocr-1995 #sequence_revision 03-Ocr-1995 #text_change 21-J C;Accession: A56098 R;Keily, R.J.; Roquine: S; Giorgi, D.; Lenzon, G.G.; Lowe, J.B. J. Biol. Chem. 270, 4640-4649, 1995 A;Itle: Sequence and expression of a candidate for the human Secret tes with the non-Secretor phenotype. A;Reference number: A56098; MUID:95181460; PMID:7876235 A;Status: preliminary A;Molecule type: DNA A;Residues: 1343 <kel> C;Genetics: CB:U17894; NID:9687618; PIDN:AAC24453.1; PID:968</kel>  | 00<br>; transmembrane protei  | FH   | LQQRIVKLQDLSEKELPMTTQMSSGNTESPEMRDSEQHGNGELRGMFTINSIGRLGNQM:   :  :  :  :  :  :  :  :  :  :  :  : | GEYATLFALARMIGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWKEER<br> | YRHIPGHFVRFTGYPCSWTFYHHLRPELLKEFTLHDHVREBAQAFLRGLRVNGSQPSTFV<br>        : | GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMARCRENINAS | RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGINAAYLAGGDTIYLANYTLPDSPF<br> | _5   |
| se Sec2, long f an) nce_revision 03 i Glorgi, D.; 649, 1995 ession of a can phenotype. ; MuID:95181460   | 0619; OMIM:182100<br>313.3<br>301gi apparatus;  | 73.1%; Score 1:<br>79.1%; Pred. No<br>ive 26; Misma  | PMTTQMSSGNTESPEN<br>  :   :<br>  volume   | AFIPASMHNALAPIFF<br>   | SWTEYHHLRPEILKEB<br>  | «KGVVADRGYLEKALI<br>   | DFALLTOCNHTIMTI<br>  | PADLSPLLK 326<br>        <br> AADLSPLLK 342                                |
| fucosyltransfera Homo sapiens (m -Oct-1995 #seque n: A56098 A., Rouquier, S hem. 270, 4640-4 equence and expr en non-Secretor e number: A56098 preliminary type: DNA : 1-343 KEL>  | A,Gene: GDB:FUT2; SE<br>A,CTCSS references: GDB:120619;<br>A,Map position: 19q13.3-19q13.3<br>C;Keywords: 91ycoprotein; Golgi | Query Match 73.1%: Score 1386.5; DB 2; Best Local Similarity 79.1%; Pred. No. 1.3e-108; Matches 258; Conservative 26; Mismatches 31; | JOORIVKLOPLSEKEL)<br>   | SEYATLFALARMNGRL/<br>  | RHIPGHFVRFTGYPCS<br>  | VHVRRGDYVHVMPNVV<br>   | GDVVFAGNGIEGSPAK<br>   | LKVFKPEAAFLPEWYGIPADLSPLLK<br>  :           <br> KIFKPEAAFLPEWTGIAADLSPLLK |
| RESULT 1 A56098 C; Species: 2 C; Date: 03 C; Accession R; Kall III C; And III | V.Gene: GDE<br>V.Cross-rei<br>V.Map posit   | Query Mat<br>Best Loca<br>Matches  | QY 1 I<br>:<br>Db 28 v  | Oy 61 G<br>Db 77 G   | Qy 121 Y<br> <br> <br> Db 137 Y   | Oy 181 G<br> <br> <br>  Db 197 G                             | Qy 241 R<br>Db 257 H   | Qy 301 L<br>Db 317 L   |

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galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) B - rat (fragment)
Nyllernate names: alpha-1.2-fucosyltransferase
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Dec-1994 #sequence_revision 23-Peb-1996 #text_change 08-Oct-1999
C;Date: 26-Dec-1994 #sequence_revision 23-Peb-1996 #text_change 08-Oct-1999
R;Piau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
Blochem. J. 300, 623-626, 1994
A;Title: Evidence for two distinct alpha-(1,2)-fucosyltransferase genes differentiall
A;Reference number: S46493; MUID:94280382; PMID:8010942
A;Accession: S46494
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a human GDP-L-fucose:beta-D-g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL 262
                                                                                                                                                                                                                                                                                                                                 macroside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) - human
C.Species: Homo sapiens (man)
C.Species: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 RPEILKEFTLHDHVREBAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
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                                                                                                          NGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFXPEA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNOMGEYATLFALARMNGRLAFIPASMH 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 TOCNHTIMIIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 YVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAG
                       A;Molecule type: mRNA
A;Residues: 1-565 CLAR>
A;Cross-references: GB:M35531; NID:9183887; PID:9306830
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  R; Larsen, R.D.; Ernst, L.K.; Nair, R.P.; Lowe, J.B. Proc. Natl. Acad. Sci. U.S.A. 87, 6674-5678, 1990 A; Title: Molecular cloning, sequence, and expression of A; Reference number: A36047; MUID:90370848; PMID:2118655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.5%; Score 1051.5; DB : 63.3%; Pred. No. 1.8e-80; tive 37; Mismatches 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 195; Conservative
                                                                                                                                                                                                              309 AFLPEWVGIPADLSPL 324
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Best Local Similarity
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                                                                                                     249
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                                                                                                   R;Hitoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
J. Biol. Chem. 270, 8844-8850, 1995
A;Title: Molecular cloning and expression of two types of rabbit beta-galactoside alphal
A;Reference number: A56392; MUID:95238380; PMID:7721792
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C.Species: Oryccolagus cuniculus (domestic rabbit)
C.Date: 19-Oct-1995 *sequence_revision 19-Oct-1995 *text_change 05-Nov-1999
C.Accession: A56392 *Kusunoki, S.; Kanazawa, I.; Tsuji, S.
R.Hitoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
A.Title: Molecular cloning and expression of two types of rabbit beta-galact
A.Reforence number: A56392; MUID:95238380; PMID:7721792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta-galactoside alphal, 2-fucosyltransferase II - rabbit
Cspecies: Oryctolagus cuniculus (domestic rabbit)
Cspecies: Oryctolagus cuniculus (domestic rabbit)
Cspecies: 19-Oct-1995 *sequence_revision 19-Oct-1995 *text_change 05-Nov-1999
Cspeciesion: B56392
Rshitoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 IPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 LRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVV 225
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                                                                                                                                                                                                                                                                                     A;Cross-references: GB:X80225; NID:9854356; PIDN:CAA56512.1; PID:9854357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGG
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                                                                                                                                                                                                                                                                                                                                                        Length 354;
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                                                                                                                                                                                                                                                                                                                                                        68.1%; Score 1291; DB 2; Length 3 83.9%; Pred. No. 1.4e-100; iive 20; Mismatches 25; Indels
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A56392
beta-galactoside alphal,2-fucosyltransferase I - rabbit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.3%;
                                                                                                                                                                                                                                                                                                                      C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 63.3%
Matches 200; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 83.9
Matches 235; Conservative
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-373 <HIT>
                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-354 <HIT>
                                                                                                                                                                                                                                     A;Status: preliminary
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C; Accession: H87311
R; anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A; Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A; Reference number: A75000; MUID:99069613; PMID:9851916
A; Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: H87911
A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-443 <STO>
A; Cross-references: GB: Chr_1; PIDN: AAC16988.1; PID: 93150470; GSPDB: GN00019; CESP: B020
C; Genetics:
        A;Title: The genes responsible for O-antigen synthesis of Vibrio cholerae 0139 are A;Reference number: Z22749; MUID:99453293; PMID:10521656
                                                                                                                                                 A;Residues: 1-281 <YAM>
A;Cross-references: EMBL:AB012857; NID:g4115688; PIDN:BAA33632.1; PID:g3721682
A;Cross-mental source: strain 022
C;Genetics:
A;Note: wblA
C;Superfamily: Vibrio cholerae hypothetical protein wblA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein B0205.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May_2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---NDWMEERYRHI-----PGHFVRFT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYPCSWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || : : : | :||||||::
112 GYWQNEQYFSQIRAVLLQELWPNQPLSINAQA--HQIKI---QQTHAVSIHVRRGDYLN- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 MFTINSIGRLGNQMGEYATLFALARMNG---RL---AFIPASMHNALAPIFRISLPVLHS 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 ------PWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKE-FTLH 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 ASKITLTSCCAYRNLSTILFNDSRI-----IERIDGYFONFRYRHPDSCKIVKKLFTFM 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 GSPAKDFALLTQCNHTIMTIGTFGIWAAYL-AGGDTIYLANYT------LPDS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---IDDLMLMCQCQHNIVANSSFSWWAAWLNSNVDKIVIAPKTWMAENPKGYKWVPDS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 DIANED--EIFHLKGSSNRLSRILRRLGWLKKNTYYAEKQRTIYDVSVFMQAPRY---LD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 MPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIE
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                                                                                                                                                                                                                                                                                                                                                               Length 281;
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                                                                                                                                                                                                                                                                                                                                                         11.3%; Score 214.5; DB 2; 26.5%; Pred. No. 2e-10; live 50; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.7%; Score 183; DB 2; L/Best Local Similarity 20.6%; Pred. No. 1.6e-07; Matches 72; Conservative 53; Mismatches 128;
                                                  A; Accession: T44328
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Matches 79; Conserv
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C;Species: Vibrio cholerae
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 28-Jul-2000
C;Accession: T44328
R;Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.
Gene 237, 321-332, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 17-Nov-1995 #text_change 08-Oct-1999
C;Date: 07-May-1995 #sequence_revision 17-Nov-1995 #text_change 08-Oct-1999
C;Accession: S51882; A44433
R;Piau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
A;Reference number: S51882
A;Reference number: S51882
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residus: 1-142 cPlAA
A;Residus: 1-142 cPlAA
A;Cross references: EMBE:L26009; NID:g414814; PIDN:AAB41514.1; PID:g554438
B;Piau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
A;Title: Evidence for two distinct alpha-(1,2)-fucosyltransferase genes differentially A;Reference number: S46493; MJD:94280382; PMID:8010942
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A,Residues: 1-159 <PIA>
A)Cross-references: EMBL:L26010; NID:g414816; PIDN:AAB41515.1; PID:g414817
C;Genetics:
A)Gene: FTB
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                         PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVN--GSQPSTFVGVHVRRGDYVHV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIE 252
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                          195 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                         Length 159,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 142;
                                                                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 VGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 353
                                                                                                                                                                         Score 846; DB 2;
Pred. No. 1.1e-63;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.6%; Score 581; DB 2; Best Local Similarity 73.2%; Pred. No. 1.5e-41; Matches 104; Conservative 15; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:L26009
C;Keywords: glycosyltransferase; hexosyltransferase
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                                                                                                                                                                         Query Match
Best Local Similarity 99.4%;
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 9-135 <PI2>
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RESULT 7 T44328

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171 V----NGSQ----

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394

RESULT 9

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A)Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-348 < SAMA
A;Cross-references: EMEE:AF016654; PIDN:AAB66030.1; GSPDB:GN00020; CESP:C17A2.4
A;Experimental source: strain Bristol N2; clone C17A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AF024500; PIDN:AAB70365.1; GSPDB:GN00023; CESP:K06H6. A;Experimental source: strain Bristol N2; clone K06H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 5
A;Introns: 17/1; 32/2; 58/1; 111/3; 150/3; 184/2; 218/1; 243/3; 272/1; 303/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein KO6H6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
C;Accession: T32294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 ---DFLDDSSQDF--GNLPRSNQRTHVTCVHARRGDFVDV-----GFQAADPDFIRNSV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 AKKI---PWQ-----NYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 TLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGV-VADRGYLEKAL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 DMFRARYSSPV-----FVVTSNGMAWCR---EN--INASRGDVVFAGNGI--EGSPA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 SIGRLGNQMGEYATLFALARMNGR--LAFIPASMHNALAPIFRISLP-----VLHSDT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 KYIAENFIPEIEYKKVHRKVVIFGDDLEFMRSLFENSVVSTDEPEYMFPAEYYISONSPA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 SGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLA--FIPA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 2
A;Introns: 94/3; 133/3; 168/2; 272/1
C;Superfamily: Caemorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                8.1%; Score 154; DB 2; Length 348; 22.8%; Pred. No. 3.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

8.1%; Score 153.5; DB 2; Length
Best Local Similarity 22.8%; Pred. No. 3.3e-05;
Matches 77; Conservative 50; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;David, M.; Wohldmann, P.; Bauer, C.; Clarke, K. submitted to the EMBL Data Library, September 1997 A;Description: The sequence of C. elegans cosmid K06H6. A;Reference number: 221147
A, Description: The sequence of C. elegans cosmid C17A2. A, Reference number: 221098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A/Accession: T32294
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-335 < DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :[ | | : :: | | | | : :: 256 EDLIYSKQNCDIVLISAPKSTFGWWIGYFSKGNKVF 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 KDFALLTQ-CNHTIMTI--GIFGIWAAYLAGGDTIY 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP: K06H6.6
                                                                                                                                                                                                                                                     A; Gene: CESP:C17A2.4
                                                           A; Accession: T31916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule, type: DDA: A; Residues: 1-363 <WIL>A; Residues: 1-363 <WIL>A; Cross-references: EMBL: 292830; PIDN: CAB07352.1; GSPDB: GN00023; CESP: F11A5.5 A; Experimental source: clone F11A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C17A2.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
C;Accession: T391916
R;Sammons, L: Wohldmann, P.
submitted to the EMBL Data Library, July 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F11A5.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 SIGRLGNQMGEYATLFALARMNGRLA--FIPASMH-----NALAPIFRISLPVLHSDT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSPAKDFALL-TQCNHTIMTI--GTFGIWAAYLAGGDTIYLANYTLPDSPFLK----- 302
                                                                                                                                                                                                           217 DPVRKRVSFWNIIYWNIHPTNHRKKPEKSTVSIFSFVTFQLRVDEFLENVGISLTVRNAR 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 NSPADDLLYAKSNCDVVLITAAHSTFGWMMGYFSKGNRVY---YT--DIQFTKDWILETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 ILHDHVREEAQAFLRGLRVNGSQPSTFVG-VHVRRGDYVHVMPNVWKGV-VADRGYLEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 LNLISRQVAKRANTAT-------VFFGDDYEFMDSLRNRTSKINAFVSQ
                                                           -----PSIFVGVHVRRGDYVHV--MPNVWKGVVADRGYLEKAL
                                                                                              212 DMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Map position: 5
A:Introns: 42/1; 55/2; 136/3; 175/3; 210/2; 243/1; 299/1; 330/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 363;
                                                                                                                                                                                                                                                                                     272 IGTFGIWAAYL---AGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGI 317
                                                                                                                                                                                                                                                                                                                            211 LDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.0%; Score 170.5; DB 2
23.4%; Pred. No. 1.4e-06;
tive 45; Mismatches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Accession: T20745
R:Gardner, A.
R:bullted to the EMBL Data Library, March 1997
A; Reference number: 219319
A; Accession: T20745
A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 23.4 Matches 73; Conservative

Query Match

CESP:F11A5.5

Genetics:

103 AKKIPWQNYH---

g QΫ́ qq Ω qq  $\delta$ g  $\nabla$ QQ 19;

Gaps

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A;Map position: 1
A:Introns: 16/1; 51/3; 77/1; 131/3; 170/3; 209/2; 244/1; 269/1; 297/3; 324/1; 354/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A)Cross-references: EMBL:299710; PIDN:CAB16868.1; GSPDB:GN00019; CESP:F08A8.5
A)Experimental source: clone F08A8
                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein FO8A8.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |: |::| | :| | :| | 305 TPEIDLAFSRIFCDVTLITAPSSTFGWWLSYLAKRTATTYYRDILESKDGVAGEMHPEDF 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 -- MEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVRE-EAQAFLRGLRVNG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 GMAWCRENINASRGDVVFAGNGIEGSPAK-------DF-----ALLTQ-- 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----DIHFAYTVFEDRVAHFTFLQKPVNNSYDYSLPQISPSYTAILTPTL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------CNHTIMII--GTFGIWAAYLAGGD-TIYLANYTLPDSPFLKVFKPEAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 INATHPSFIETLNRNIQPLF----PKLADQFTLRIIPDSLVTHQQTNWGRCCVYDDPSRF 154
                                                                                                                                                                                  230 --MAWCREN-----INASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTI--GTFGIW 278
                                                                                                                                                                                                                 235 PFMKNLYENESTHFVSVNSPSDDLVYAKN-------NCDTVLITAPHSTFGWW 280
                                             141 YLHLDGRFYQ-----AWKYFPSMRNELI------GYLKTSENFGSLPKSNE 180
                                                                                          STFVG-VHVRRGDYVHVMPNVWKGVV-ADRGYLEKALDMF--RARYSSPVFVVTSNG--- 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 QMSSGNTESPEMRRDSEQHGNGE--LRGMFTINSIGRLGNQMGEYATLFALARMNGRLAF 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 IPA-----SMHNALAPIFRISLPVLHSD-TAKKIP--WQNYHLNDW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 SQPSTF----VGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSN
                                                                                                                      121 YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.4%; Score 139.5; DB 2; Length 383; Best Local Similarity 21.7%; Pred. No. 0.00059; Matches 81; Conservative 52; Mismatches 135; Indels 105;
                                                                                                                                                                                                                                                                                                                       281 MGYFSKGDKVYYMDIRETRDNVYRNGGLNPYDYYLPHW 318
                                                                                                                                                                                                                                                                            279 AAYLAGGDTIYLANY-TLPDSPFLK-VFKPEAAFLPEW 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Harris, B. Submitted to the EMBL Data Library, October 1997 A: Reference number: 219294 A: Accession: T20572 A: Status: preliminary: translated from GB/EMBL/DDBJ A: Modecule type: DNA A: Residues: 1-383 <WIL>
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XPPEWIKLKTDLN 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T20572
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T22068
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probable alpha(1,2)fucosyltransferase - Helicobacter pylori (strain J99)
C.Species: Helicobacter pylori
A:Variety: strain J99
C.Cate: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000
C.Cates: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000
C.Catesion: H71976
C.Adm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F. Nature 397, 176-180, 1999
A.Title: Genomic sequence comparison of two unrelated isolates of the human gastric p. A; Reference number: A71800; MuID:99120557; PMID:9923682
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A)Experimental source: strain J99
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hypothetical protein F41D3.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T22068  
R;White, S. submitted to the EMBL Data Library, November 1996  
A;Reference number: 219508  
A;Accession: T22068  
A;Accession: T22068  
A;Accession: T22068  
A;Actus: preliminary; translated from GB/EMBL/DDBJ  
A;Accession: 1500  
A;Accession: T2000  
A;Accession: T2000 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 KGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 DFALL------TYLONHTIMTI--GTFGIWAAYLAGGDT-IYLANY-TLPDS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 MTIVYKGGLGNQLFEVLSLLGIARKLKRIA-----VFNSSDPVLQSNLEFLNQKLPRIS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Map position: 1
A;Introns: 23/1; 59/1; 112/3; 150/3; 222/1; 278/1; 308/3; 326/3; 421/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 MFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFR---
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C;Superfamily: Vibrio cholerae hypothetical protein wblA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.3%; Score 138.5; DB 2; Best Local Similarity 23.4%; Pred. No. 0.001; Matches 74; Conservative 48; Mismatches 105;
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A; Residues: 1-299 <ARN>
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A;Map position: 5
A:Introns: 50/1; 80/2; 140/3; 179/3; 218/2; 253/1; 278/1; 306/3; 325/1; 342/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Residues: 1-365 <WIL>
A.Residues: 1-365 <WIL>
A.Cross-references: EMBL: Z81132; PIDN: CAB03434.1; GSPDB: GN00023; CESP: T26E4.4
A: Experimental source: clone T26E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T26E4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: T25309
                                                                                                                                                                                                                                                                                                                                                  260
                                                                                                                                                                                                                                                                     -----LLTQCNHTIMTIGTFGIWAAYLAG--GDTIYLANYTLPDSPFLKVFKPEAAF 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 EEAYWDMLLMQSCKHGIIANSTYSWWAAYLINNPGKIII------GPKHWLFGHENIL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 GNQMGEYATLFALARMNGRLAFIPA-----SMHNALAPIFRISLPVLHSDTAKKIPWQ 109
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                                                                                                              --LPVLHSDTAKKIPWQNYHLNDWMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKE 151
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                                                    10 GGLGNQMFQYAFAKSLQKHSNTPVLLDITSFDGSNRKMQLELFPIDLPYASAKEIAIAKM 69
GRLGNQMGEYA-------TLFALARMNGRLAFIPASMHNALAPIFRIS--
                                                                                                                                                                                                                             152 FTL----HDHVREEAQAFIRGLR-VNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRG
                                                                                                                                                                                                                                                                                                                                                  206 YLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFA----
                                                                                                                                                                                                                                                                                                                                                                                       GDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 295
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----ESHFEVKSQ 295
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                                                                                                                                              112892 seqs, 41476328 residues
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| CN3B_MOUSE YFAS_ECOLI GLO2_SYNY3 GLO2_SYNY3 DPOL_ADE04 CTAl_HUMAN GRB2_XENLA RIBB_HELPJ SUIS_RAT Y285_MYCGE CTAl_MOUSE   | ALIGNMENTS | PRT; '340 AA.                              | 1)  quence update) notation update) ferase 2 (EC 2.4.1.69) ( syltransferase 2) (Alpha | Craniata; Vertebrata;<br>dactyla; Suina; Suidae; | N 11)  SEQUENCE FROM N.A.  MEDLINE=97468270; PubMed=9321466;  A Meijerink E., Fries R., Voegeli P., Masabanda J., Wigger G.,  A Stricker C., Neuenschwander S., Bertschinger H.U., Stranzinger G.;  Two alpha(1,2) fuccsyltransferase genes on porcine chromosome 6cl  T are closely linked to the blood group inhibitor (S) and Escherichi  Coli F18 receptor (ECFERR) loci.";  Mamm. Genome 8:736-741(1997). | 12) SEQUENCE FROM N.A. Cohney S., Mouhtouris E., McKenzie I.F.C., Sandrin M "Molecular cloning and characterization of the pig se alpha(1,2) floosyltransferase."; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databas | N.A.<br>the EMBL/GenBank/DDBJ databa | ND 316-334.<br>2879;<br>M.;<br>GDP-L-fucose: beta-D-gal | is likely a counterpart<br>group transferase.";<br>80(1995).<br>L-fucose + beta-D-galact<br>-D-galactosyi-R. | PE II MEMBRANE PROTEIN.<br>OF GOLGI (BY SIMILARITY) | This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation CC the Buropean Bioinformatics Institute. There are no restrictions on it cuse by non-profit institutions as long as its content is in no war modified and this statement is not removed. Usage, by and for commercial contents a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch). |
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15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
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                                                                                                                                                         SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                           LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

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                            EMBL, AF027304; AAC09170.1; -.
EMBL, X99621; CAA67932.1; -.
Interpro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Golgi stack; Signal anchor.
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                                                                                                                                      CYTOPLASMIC (POTENTIAL)
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81.9%; Pred. No. 1.5e-113;
tive 26; Mismatches 19;
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340 AA;
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01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 34, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-1-fucosyltransferase 2) (Alpha(1,2)FT 2)
(Fucosyltransferase 2) (Secretor blood group alpha-2-
fucosyltransferase) (Secretor factor) (Se) (SE2).
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 LHQRLEKMQPTWELEA-----LEPATMETPSRPQPRPQLKGWWTINAIGRLGNQM 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                 LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

F35AC33F1B7B9F68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                   Interpro; IPR002516; GT_11.
Pfam; Pf0131; G1yco_transf_11; 1.
Transferase; G1ycosyltransferase; G1ycoprotein; Transmembrane; G01g1 stack; S1gnal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata;
Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.5%; Score 1393; DB 1; 78.8%; Pred. No. 2.1e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 AA
                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
MEDLINE=95181460; PubMed=7876235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39320 MW;
                                                                                                                                                                                                                EMBL; X99620; CAA67931.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                      344
189
255
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUT2_HUMAN
Q10981;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL), SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN). LUMENAL, CATALYTIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: CREATES A SOLUBLE PRECURSOR OLIGOSACCHARIDE FUC-ALPHA ((1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN ESSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE SOLUBLE A AND B ANTIGEN SINTHESIS PATHWAY. H AND SE BNZTMES FUCOSYLATE THE SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KN VALUES.

CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
"Sequence and expression of a candidate for the human Secretor blood group alpha(1,2)fucosyltransferase gene (FUT2). Homozygosity for an enzyme-inactivating nonsense mutation commonly correlates with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTHRAY: GLYCOSYLATION
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY THE USE OF
ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
TISSUE SPECIFICITY: SMALL INTESTINE, COLON AND LONG.
MISCELLARBOUS: THERE ARE TWO GENES (FUTI AND FOTZ) WHICH ENCODE
GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THER ARE EXPRESSED IN A
TISSUE-SPECIFIC MANUER WITH EXPRESSION RESTRICTED TO CELLS OF
MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                               Kudo T., Iwasaki H., Nishihara S., Shinya N., Ando T., Narimatsu I.,
                                                                                                                                                                                                     "Molecular genetic analysis of the human Lewis histo-blood group
System. In. Secretor gene inactivation by a novel single missense
mutation A385T in Japanese nonsecretor individuals.";
J. Biol. Chem. 271:9830-9837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             du Toit E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GALACTOSIDE 2-L-FUCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GALACTOSIDE 2-L-FUCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: JPR002516; GT_11.
Pfam: PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack; Alternative initiation;
Blood group antigen; Polymorphism:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Extensive polymorphism of the FUT2 gene in an African (Xhosa)
                                                                                                                                                                                                                                                                                                                                        Koda Y., Soejina M., Wang B., Kimura H.;
"Structure and expression of the gene encoding secretor-type
galactoside 2-alpha-L-fucosyltransferase (FUT2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu Y., Koda Y., Soejima M., Pang H., Schlaphoff T.,
Kimura H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHORT ISOFORM.
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                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANT PHE-140.
MEDLINE-97363210; PubMed=9219535;
                                                                                                                      SEQUENCE FROM N.A., AND VARIANT PHE-140.
MEDLINE=96199252; PubMed=8621666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS VAL-25; CYS-138 AND ASN-172.
                                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Biochem. 246:750-755(1997).
                                                           non-secretor phenotype.";
J. Biol. Chem. 270:4640-4649(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98431007; PubMed=9760207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  f South Africa.";
103:204-210(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U17894; AAC24453.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D87942; BAA21684.1; -.
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Hum. Genet. 10
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                                                                                                                                                                                    Narimatsu H.;
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DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAX-2000 (Rel. 39, Created)
30-MAX-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
(Fucosyltransferase 2) (FUT-III).
                                                                                                                                                                                                                                                                                                                                                            241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYILPDSPF 300
                                                                                                                                                                                                                                                                                                                                             GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                                                                                                                                                                                                                                                         YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 HGDVVFAGDGIEGSPAKDFALLIQCHHIMIMIMIGTFGIWAAYLIGGDTIYLANYTLPDSPF 316
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                         28 VQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGMWIINAIGRLGNWM 76
                                                                                                                                                                                                                                                                                 1 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEWRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S.;
Modecular cloning and expression of a mouse GDP-L-Fucose: beta-D-
galactoside 2-alphar-P-Fucosyltransferase ";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 GVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTS
                                                                                                              -> F (IN JAPANESE SEJ ALLELE; NON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
N-LINKED (GLCNAC. .) (POIENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                     11;
                                  (POTENTIAL)
                                                                                                                                                                                                                      DB 1; Length 343;
                                             I -> V (IN XHOSA POPULATION)...
/FTIG=VAR_003422.
R -> C (IN XHOSA POPULATION).
/FTIG=VAR_003423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ICR: TISSUE=Gastrointestinal tract;
Lin B., Hayashi Y., Saito M., Sakakihara Y., Yanagisawa M.
                                                                                                                                                        D -> N (IN XHOSA POPULATION)./FTId=VAR_003425.
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                       12056D9CF175E13A CRC64;
                                                                                                                                                                                                                     Score 1386.5; DB 1;
Pred. No. 7.3e-110;
6; Mismatches 31;
                                                                                                                                             /FTId=VAR_003424.
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                                                                                                                           SECRETOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 LKIFKPEAAFLPEWTGIAADLSPLLK 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                       343 AA; 39017 MW;
                                                                                                                                                                                                                73.18;
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                                                                                                           140
                                                                              138
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                                                                                                                                                                                                                                   Best Local Similarity
Matches 258; Conserv
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 188
282
308
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P97353;
                CARBOHYD
CARBOHYD
   CARBOHYD
                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                      Query Match
                                                                              VARIANT
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                                                VARIANT
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NCBI_TaxID=9986;
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                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as along a sits content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
PATHWAY: Glycosylation: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND SEC1) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-007-1996 (Rel. 34, Created)
01-007-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (Secretor blood group alpha-2-fucosyltransferase) (GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase 2) (Alpha(1,2)FT 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGXLEKALDMFRARXSSPVFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
LUMBRAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                        EMBL, AF11352, CAN125351.1;
MGD: MGI:109374; Fut2.
Interpro; IPR002516; GI.
Pfan: PF01531; GIYCo_transf.ll; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4093E853EB37303B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.6%; Score 1338; DB 1;
88.0%; Pred. No. 9.9e-106;
tive 16; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIIXLANYTLPDSPFLKVFKPEAAFLPEWVGIPADL 321
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                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41464 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stack.
                                                                                                                                                                                                                                                                                                                                                           EMBL; Y09882; CAA71008.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368
195
289
315
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195
289
315
368 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal-anchor;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUT2_RABIT
Q10983;
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CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUT2_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the Buropean Bioinformatics Institute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 GMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                      FUCOSYLATE THE SAME ACCEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                               Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S.;
"Molecular cloning and expression of two types of rabbit beta-
"Molecular cloning and expression of two types of rabbit beta-
galactoside alpha 1,2 fucosyltransferase.";
J. Biol. Cham. 270:884 8850(1955).
-!-FUNCTION: CREATES A SOLUBLE PRECURSOR OLIGOSACCHARIDE FUC-ALPER
((1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN ESSENTIAL
SUBSTRATE FOR THE FINAL STEP IN THE SOLUBLE A AND B ANTIGEN
SYNTHESTS PATHWAY. H AND SE ENZYMES FUCOSYLATE THE SAME ACCEPTOR
SUBSTRATES HOT EXHIBIT DIFFERENT KM VALUES.
-!-CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +
alpha-L-fucosyl-1,2-beta-D-galactosyl-R = GDP +
                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: GIYOSYJATION.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CLSTERNAR OF GOLGI.
-!- TISSUE SPECIFICITY: SALIYARY AND LACTATING MAMMARY GLANDS.
-!- MISCELLANGOUS: THERE ARE TREE GENES (FUT1, FUT2 AND FUT3) WHICE ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE IN RABBIT. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 IPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAF
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

1E2B831F9DA6CCB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.1%; Score 1291; DB 1; 83.9%; Pred. No. 8.9e-102; ive 20; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
                                                      MEDLINE=95238380; PubMed=7721792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40035 MW;
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197
291
317
354 AA;
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Matches 235; Conserv
SEQUENCE FROM N.A.
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DOMAIN
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FUT1 RAT
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                                                                       225
                                                                                                                                    249
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                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATHWAY: GLYCOSYLATION.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
TISSUE SPECIFICITY: IN THE ADULT, HIGHLY EXPRESSED IN PANCREAS,
TESTIS AND EPIDIDYMIS AND TO A LESSER EXTENT IN THYMUS, LONG,
TOWACH, SMALL INTESTINE, COLON, SPLEEN AND UTERUS. NOT EXPRESSED
IN BRAIN, HERRY, SKELETAL MUSCLE, KIDNEY, LIVER AND BONE MARROW.
MISCELLANGOUS: THERE ARE TWO GENES (FUTL AND FUT2) WHICH ENCODE
GALACTOSIDE 2-L-FUCOSYLTRANSFERASE.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LUMENAL, CATALYTIC (POTENTIAL).
LUNED (CLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
21F1D24CFE204106 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 ARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 AQLNGRQAFIQPEMHAALAPVFRISLPVLDPEVDSLIPWQHLVLHDWMSEEYSHLEDPFL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 RFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPS-TFVGVHVRRGD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. J. 327:105-115(1997).
-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STEAIN=NIH Swiss;
MEDLINE-97454449; PubMed=9355741;
Domino S.E., Hiraiwa N., Lowe J.B.;
"Molecular cloning, chromosomal assignment and tissue-specific expression of a murine alpha(1,2)fucosyltransferase expressed i thymic and epididymal epithelial cells.";
Biochem. J. 327:105-115(1997).
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Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
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      376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.3%; Score 1105.5; 62.8%; Pred. No. 4.5e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 SI
376 LU
67 N-
302 N-
42255 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U90553; AAC53492.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Golgi stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .09375; Fut1.
IPR002516; GT_11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
      STANDARD;
                                                                                                                                                                                                                           (Fucosyltransferase 1).
                                                                                                                                                                                                                                                                                  musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 3
67 302
302 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:109375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal-anchor;
DOMAIN
FUT1_MOUSE 009160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Sin
ses 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piau J.-P., Labarriere N., Dabouis G., Denis M.G.;

Evidence for two distinct alpha(1,2)-fucosyltransferase genes
differentially expressed throughout the rat colon.";
Biochem. J. 300:623-626(1994).

-!-CATALYTIC ACTIVITY. GDP-L-fucose + beta-D-galactosyl-R = GDP +
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.

-!-PATHWAY: Glycosylation.
-!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILERITY).

-!- GLACTOSIDE 2-L-FUCOSYLTRANSFERASE THEY ARE EXPRESSED IN A
TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF
MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.

-!- SIMILARITY: BELONGS TO THE GLXCOSYLTRANSFERASE FAMILY II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1.2)FT 1)
YVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAG 248
                                            NGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEA 308
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIÂL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; Glycosyltransferase; Glycoprotein; İqansmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soejima M., Wang B., Koda Y., Kimura H.;
"Two distinct rat GDP-L-fucose:b-D-galactoside 2-alpha-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fucosyltransferase genes.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 AA
                                                                                                                                                                                                                                                                                                            AFLPEWVGIPADLSPLLKALTPACPRSHFHL 339
                                                                                                                                                                                                                                                                                                                                                                                345 AFLPEWVGINADLSPLQAQFDPWKPDSLFRL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L26009; AAB41514.1; -.
InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94280382; PubMed=8010942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB015637; BAA31130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 169-310 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAA21741.1;
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DOMAIN 1 12
TRANSMEM 13 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Fucosyltransferase 1). FUT1 OR FIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Colon cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116
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RESULT
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01-0CT-1996 (Rel. 34, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2-4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
                                                                                                                                                                                                                                                                            70 ARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFV 129
                                                                                                                                                                                   187
                                                                                                                                                                                                      223
                                                                                                                                                                                                                           247
                                                                                                                                                                                                                                                                 GNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPE 307
                                                                                                                                                             104 AQINGRRAFIQPEMHITLAPVFRISLPVLDPEVDSLIPWQHLVLHDWMSEEYSHLEDPFL 163
                                                                                                                      PVAMVCLPYPSNASSGSPSCPE------OSLLSGTWTITPGGRFGNOMGQYATLLAL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 RFIGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVN--GSQPSTFVGVHVRRG
                                                                                                                                                                                              DYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFA
                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                    PLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFAL
  LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

C350C737C758B7F8 CRC64;
                                                                                11;
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                                                           Length 376;
                                                           58.1%; Score 1101.5; DB 1; Length 62.3%; Pred. No. 9.8e-86; Live 37; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                373 AA
                                                                                                                                                                                                                                                                                                                       344 AAFLPEWVGINADLSPLQAQFDPWETDSLFRL 375
                                                                                                                                                                                                                                                                                                           AAFLPEWVGIPADLSPLLKALTPACPRSHFHL 339
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95238380; PubMed=7721792;
                                           ..
Σ
                                                                                   207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fucosyltransferase 1).
    376
64
302
328
    30
64
302
328
376 AA;
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                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUTI OR RFT-I.
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    DOMAIN
CARBOHYD
CARBOHYD
                                                               Query Match
                                  CARBOHYD
                                          SEQUENCE
                                                                          Best Local
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                                                                                                                                                                                                                                                                                                                                                              RESULT 8
FUT1_RABIT
                                                                                                                                                                                                                                                 224 1
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                noved. Usage by and for commercial (see http://www.isb-sib.ch/announce/
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JNN-2002 (Rel. 41, Last annotation update)
6alactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
(Fucosyltransferase 1) (Blood group H alpha 2-fucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 YVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 NGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Larsen R.D., Ernst L.K., Nair R.P., Lowe J.B.; "Molecular cloning, sequence, and expression of a human GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase cDNA that can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 LPMTTQMS-----SGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 FTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LUMBNAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL)

N-LINKED (GLCNAC...) (POTENTIAL)

N-LINKED (GLCNAC...) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                         57.0%; Score 1080.5; DB 1; Length 373; 63.3%; Pred. No. 5.8e-84; ive 44; Mismatches 51; Indels 21;
                                                                                                                       Interpro: IPR002516; GT_11.
Pfam: PF01331; G1yco_transf_11; 1.
Transferase: G1ycosyltransferase; G1ycoprotein; Transmembrane: Signal-anchor; G01g1 stack.
    as its content. Usage by an
                                                                                                                                                                                                                                                                                                                                      0A47A1786231525C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H blood group antigen.";
    use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See hor send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A., AND VARIANT ALLELES
                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90370848; PubMed=2118655;
                                                                                                                                                                                                                                                                                                                                              M.
                                                                                                                                                                                                                                                                                                                                            42098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 AFLPEWVGIPADLSPL 324
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 200; Conservative
                                                                                                      EMBL; X80226; CAA56513.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                              30
66
301
327
373 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                         737
                                                                                                                                                                                      Signal-anchor;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUT1_HUMAN P19526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              form the
                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koda Y., Soejima M., Johnson P.H., Smart E., Kimura H.;

Missense mutation of FUT1 and deletion of FUT2 are responsible for
Indian Bombay phenotype at ABO blood group system.";

Biochem. Blophys. Res. Commun. 238:21-25(1997).

-!- FUNCTION: CREATES A SOLUBLE PRECURSOR OLIGOSACCHARIDE FUC-ALPHA

((1,2)GALBERA-) CALLED THE HARNIEGE SANESENTIAL

SUBSTRAIRE BOT EFIRM. STEP IN THE SOLUBLE A AND B ANTIGEN

SUBSTRAIRE BOT EXHIBIT DIFFERENT KW VALUES.

-!- CATALYICA ACTIVITY: GDP-1-fucose + beta-D-galactosyl-R = GDP +

alpha-L-fucosyl-1,2-beta-D-galactosyl-R.

-!- PATHEMY: Gly-CALION: TYPE II MEMBRANE FROTEIN. MEMBRANE-BOUND

FORM IN TRANS CISTERNAE OF GOLGI.

-!- POLLWARPHIGN. NONFUNCTIONAL MUTANT OF FUT1 ARE THE CAUSE OF THE H-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACYOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERMAL OR ENDODERNAL ORIGIN RESPECTIVELY.
                                                                                                                                                                                                                                                                                   Molecular basis for H blood group deficiency in Bombay (Oh) and
                                                                                                                                                                                                 MEDLINE-94286534; PubMed-7912436;
Kelly R.J., Ernst L.K., Larsen R.D., Bryant J.G., Robinson J.S.
Lowe J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harn, 201531; Glyco_transf_11; 1.

Pfam: PF01531; Glyco_transf_11; 1.

Pfam: PF01531; Glyco_transf_11; 1.

Signal anchor; Golgi stack; Polymorphism: Blood group antigen.

DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).

TRANSMEM 9 25 SIGNAL-ANGHOR (TYPE-II MEBRRANE PI LUMBRAL, CATALYTIC (POTENTIAL).

CARBOHYD 56 65 N-LINKED (GLCNAC. ...) (POTENTIAL).

CARBOHYD 327 327 N-LINKED (GLCNAC. ...) (POTENTIAL).
                        Wagner F.F., Flegel W.A.; "Polymorphism of the hallele and the population frequency of sporadic nonfunctional alleles."; Transfusion 37:284-290(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_003417.
L -> H (IN PARA-BOMBAY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .)
Y -> C (IN BOMBAY H-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=vAR_009708.
W -> C (IN BOMBAY H-).
/FTId=vAR_003418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V -> E (IN BOMBAY H-).
/FTId=VAR_003419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L -> R (IN BOMBAY H-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W -> C (IN BOMBAY H-).
                                                                                                                                                                                                                                                                                                                     para-Bombay individuals.";
Proc. Natl. Acad. Sci. U.S.A. 91:5843-5847(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> V (IN BOMBAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VAR_009709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR_003420
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97445117; PubMed-9299444;
MEDLINE=97240210; PubMed=9122901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M35531; AAA52639.1; -.
EMBL; Z69587; CAA93435.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGNC:4012; FUT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOMBAY BLOOD GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164
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                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT ARG-242.
                                                                                                                                                                      VARIANT HIS-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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327
154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:
MIM; 211100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
VARIANT
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RANGE STATE TO THE STATE ```

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ä
   01-Nov-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
6alactoside 2-L-fucosyltransferase 1 (RC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
  ţ0
   59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
  RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
  203 DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL 262
  Gaps
  NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 144
   TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 322
  GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 84
  Meijerink E., Neuenschwander S., Fries R., Dinter A., Meijerink E., Neuenschwander S., Fries R., Dinter A., Bertschinger H.U., Stranzinger G., Voegeli P.; Expression and activity of porcine alpha(1,2)fucosyltransferases determine erythrocyte antigen precursor O status and susceptibility to Escherichia coli FIB colonization in the small intestine... Submitted (MAR.1999) to the EMBL/GenBank/DDBJ databases.
   SEQUENCE FROM N.A., AND 'VARIANTS THR-103 AND GLN-286.
MEDILINE=94468270; PubMed=9231466;
Medijerink E., Fries R., Voegeli P., Masabanda J., Wigger G.,
Stricker C., Neuenschwander S., Bertschinger H.U., Stranzinger G.;
"Two alpha(1,2) fucosyltransferase genes on porcine chromosome 6q11
are closely linked to the blood group inhibitor ($) and Escherichia
coli F18 receptor (ECP18R) loci.";
Mamm. Genome 8:736-741(1997).
  Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
  .;
m
   DB 1; Length 365;
   Indels
  MEDLINE=96217559; PubMed=8613146;
Cohney S., Mouhtouris E., McKenzie I.F., Sandrin M.S.;
"Molecular cloning of the gene coding for pig alphal-->2
/FIId=VAR_003421.
4F4442EC375C9D9E CRC64;
  55.5%; Score 1051.5; DB 1;
63.3%; Pred. No. 1.6e-81;
ive 37; Mismatches 73;
  PRT;
                                   41251 MW;
  Immunogenetics 44:76-79(1996).
   63.3%;
   Ouery Match
Best Local Similarity 63.3%
Matches 195; Conservative
  STANDARD;
   (Fucosyltransferase
                               365 AA;
   fucosyltransferase.
  SEQUENCE FROM N.A.
   323 PLLKALIP 330
  358 PLWTLAKP 365
   SEQUENCE FROM N.A.
  Sus scrofa (Pig).
   Q29043; 019101;
01-NOV-1997 (Re.
                                   SEQUENCE
   FUT1_PIG
  25
  145
  173
   263
  RESULT 10
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SEQUENCE FROM N.A.
  NCBI_TaxID=10116;
  YKQ7_CAEEL
P34302;
   CARBOHYD
   Query Match
  NON_TER
   YKQ7_CAEEL
  RESULT 12
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  2
  SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
LUMERAL, CATALYIIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
  169
  194
  77 AFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPC 136
   NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS 254
   PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 314
  Gaps
   17 PMTTOMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRL 76
          PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI.
MISCELLANEOUS: THERE ARE TWO GENES (FUTI AND FUT2) WHICH ENCODE
   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last nanotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.59) (Secretor blood group alpha-2-fucosyltransferase) (GDP-L-fucose:beta-D-
   SWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMP
   ÷
   EMBL; U70883; AAB81884.1; -.
EMBL; AF136896; AAF59633.1; -.
Interpreto; IPR002516; GI_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
   55.4%; Score 1050.5; DB 1; Length 365; 62.9%; Pred. No. 1.9e-81;
   GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN
  TISSUE-SPECIFIC MANNER.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
  Indels
   A -> T.
R -> Q.
L -> F (IN REF. 1).
DAFCE77E89A29D75 CRC64;
   Ĝolgi stack; Polymorphism.
1 8 CYTOPLASMIC (POTENTIAL).
   159 AA.
alpha-L-fucosyl-1,2-beta-D-galactosyl-R
  Mismatches
   PRT;
  38;
  41106 MW;
   EMBL; L50534; AAB02984.1; -.
   62.9%;
  Conservative
   STANDARD;
   28
365
65
301
327
103
286
  VGINADLSPL 359
   315 VGIPADLSPL 324
   365 AA;
   Similarity
   29
65
301
327
103
286
   Signal-anchor;
DOMAIN
  195;
  FUT2_RAT
Q10984;
  CONFLICT
   TRANSMEM
   CARBOHYD
   CARBOHYD
  CARBOHYD
  Query Match
  Local
  VARIANT
  VARIANT
  DOMAIN
   Best Loca
Matches
   290
   RESULT 11
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   differentially expressed throughout the rat colon.";
Biochem. J. 300:623-626(1994).
-i- FUNCTION: CREATES A MEMBRANE.-ASSOCIATED PRECURSOR OLIGOSACCHARIDE
FUC-ALPHA((1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN
ESSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE MEMBRANE.-ASSOCIATED
A AND B ANTIGEN SYMPHESIS PATHWAY. H AND SE ENZYME FUCOSYLATE
THE SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.
   Gaps
   195 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS 254
  25 PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 314
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
   1 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDGVFAGNGIEGS 60
  -!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1.2-beta-D-galactosyl-R.

-i alpha-L-fucosyl-1.2-beta-D-galactosyl-R.

-i PATHWAY: Glycosylation:
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROFIEIN. MEMBRANE-BOJND FORM IN TRANS CISTERNAE OF GOLG! (BY SIMILARITY).

-i MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A
  ö
  N-LINKED (GLCNAC. . .) (POTENTIAL)
14DECEB7C2E6384A CRC64;
   Plau J.-P., Labarriere N., Dabouis G., Denis M.G.;
"Evidence for two distinct alpha(1,2)-fucosyltransferase genes
   Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Golgi stack.
  TISSUE-SPECIFIC MANNER.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11
3
  Score 846; DB 1; Length 159;
Pred. No. 1.4e-64;
0; Mismatches 1; Indels
galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT
   315 VGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 353
   Pred. No. 1.4e-
0; Mismatches
   365 AA
  InterPro; IPR002516; GI_11.
Pfam; PF01531; Glyco_transf_11; 1.
                         (Fucosyltransferase 2) (Fragment)
  MEDLINE=94280382; PubMed=8010942;
  1 1
98 98 N
159 AA; 17250 MW;
   44.68;
  Best Local Similarity 99.4%;
Matches 158; Conservative
   EMBL; L26010; AAB41515.1;
   STANDARD;
  Rattus norvegicus (Rat).
   FUT2 OR SEC1 OR FIB.
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VGLD_HSVEK
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  16;
  Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Faveln A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
  102 --TAKKIP------WQNYHINDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEF 152
   153 TLHDHVREEAQAFLRGL----RVNGSQPSTFVG---VHVRRGDYV---HVMPNVWKGVVA 202
   278 KYFVS---ENTPQDDLAYSHYSCDATLITAPSSTFGWWLGYLSKGQAVYYQDIRSTNDVN 334
  Gaps
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
  ပ
  ----YSSPVFVVTSNGMAWCRENINASRGD
   244 VVFAGNGIEGSPAKDFALL-TQCNHTIMTI--GTFGIWAAYLAGGDTIYLANY-TLPDSP
  224 --SFIKPALEFIKEREOKDVNKKMLTVIMGDDPDFEAKMF----EGTVRAKKEAKIEETT
  2.2 Mb of contiguous nucleotide sequence from chromosome III of
  88;
  130 HNKATKVPLSEKCCIFDNPDKFNNISSEYLHLTGHFYQ-----SWKYF-----
  Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
   8.9%; Score 168; DB 1; Length 365; 22.0%; Pred. No. 7.3e-07; ve 48; Mismatches 115; Indels
  52 SIGRLGNQMGEYATLFALARMNGR--LAFIPASMHNALAPIFRISLPVLHSD-
  Pfam; PF01531; Glyco_rransf_11; 1.
Hypothetical protein; Transferase; Glycosyltransferase.
SEQUENCE 365 AA; 41991 MW; B5FBCA363F31977F CRC64;
   STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
  300 FLK-VFKPEAAFLPEWVGIPAD 320
  22.0%;
   WormPep; C06E1.7; CE30483.
InterPro; IPR002516; GT_11
  Query Match
Best Local Similarity 22.09
  EMBL; L16559; AAA27932.2;
   Nature 368:32-38(1994).
Caenorhabditis elegans
  203 DRGYLEKALDMFRAR--
   Waterston R.;
   Wohldman P.;
  REVISIONS
  elegans
   335
  g
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  QΥ
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RESULT 13

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   10;
   Flowers C.C., Eastman E.M., O'Callaghan D.J.; "Sequence analysis of a glycoprotein D gene homolog within the unique short segment of the EBY-1 genome."; Virology 180:175-184(1991).
  109 QNYHLNDWMEERYRH----IPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQ 163
  51 NSIGRLGNOMGEYAT - LFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPW 108
  332 DNHPGFDSVESEITQNKTDPKPGQADPKPNQPFKWPSIKHLVPRL------DEVDEVIE 384
  288 RFLGEFNFPQGEHMTWVKFWFVYDGGNL---PVQFYEAQA-------FARPVƏP 331
   Gaps
   1 LQQRIVKLQ------PLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTI 50
  MEDLINE=92263758; PubMed=1316673; Colle C.F. III, Flowers C.C., O'Callaghan D.J., Colle C.F. III, Flowers C.C., O'Callaghan D.J., Copen reading frames encoding a protein kinase, homolog of allycoprotein gx of pseudorabies virus, and a novel glycoprotein within the unique short segment of equine herpesvirus type 1."; Virology 188:545-557(1992).
  164 AFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSP 223
   -! - SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.
  N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
  4.8%; Score 91; DB 1; Length 442; 22.7%; Pred. No. 2.9;
   Mismatches 103; Indels
  EXTRACELLULAR (POTENTIAL).
   Equine herpesvirus type 1 (strain Kentucky A) (EHV-1).
  323CDCA9C9762F05 CRC64;
  CYTOPLASMIC (POTENTIAL).
   Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-0c7-2001 (Rel. 40, Last annotation update)
Glycoprotein D precursor (Glycoprotein 17/18)
GD OR GP17/18 OR 72.
  N-LINKED (GLCNAC
  POTENTIAL.
GLYCOPROTEIN D.
 442 AA
  POTENTIAL
   InterPro; IPR002896; Herpes_glycop_D.
Pfam; PF01537; Herpes_glycop_D; 1.
  Transmembrane.
PRT;
   EMBL; M86931; -; NOT_ANNOTATED_CDS.
EMBL; M87497; AAA46073.1; ALT_INIT.
   SEQUENCE FROM N.A. MEDLINE=91082407; PubMed=1845821;
   31;
  49908 MW;
   EMBL; M62923; AAA45081.1;
   Conservative
 STANDARD;
   4442
4422
1103
347
  19
   Glycoprotein; Signal; Signal;
   PIR; A38518; VGBEEA.
  111
347
396
442 AA;
  Query Match
Best Local Similarity
   54;
VGLD_HSVEK
  DOMAIN
TRANSMEM
DOMAIN
  CARBOHYD
  CARBOHYD
  SEQUENCE
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  CHAIN
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us-10-040-863-10.rsp

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STRAIN-OGC101
  Divne C.;
   RESULT 15
CDH_PHACH
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   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   12;
  TFNGAYSPANYTHVDWLGROYTEIGAATVNTPKGF----YVLESTYAQNAGLRPTILC 245
  80 LITELTEGNQEAAGLIMTAEPVEVTLVAGN------NYYGYDGSQGGNQISQGTPLE 130
   Fujiwara T., Morishima S., Takahashi I., Hamada S., "Molecular cloning and sequencing of the fimbrilin gene of Porphyromenas gingivalis strains and characterization of recombinant proteins.";
   FUNCTION: Fimbrillin is the structural subunit of the fimbriae, that are filamentous appendages on the cell sufface. Fimbriae of P.gingivalis are recognized as a major virulence factor as they mediate cell adhesion and play an important role in invasion of
   Gaps
385 PVTKPPKTSKSN-STFVGISVGLGIAGLVLVGVILYVCLRR---KKELKVCTERLDSP 438
   BY SIMILARITY.
MAJOR FIMBRIAL SUBUNIT PROTEIN, TYPE
7 7FBE4FBF427EA2AB CRC64;
   : |:: |:|| | :| : | : : :: |||
IKRVHARIAFIKIEVTMSQSYANKYNFAPENIYALVAKKKSNLFGASLANSDDAYLTGSL
   18 MTTQMSSGNTESPEMRRDSEQ-----HGNGELRGMFTINSIGRLGNQMG---EYATLFA
  -----IPWQNYHLNDWMEERYRHI-----PGHFVRFTGYPCSWTFYHH--LRPEIL-
  LARMNGRLAF--1PASMHNALAPIFRISLPVLHSDTAKK-------
  Hamada S.;
"Functional differences among FimA variants of Porphyromonas
gingivalis and their effects on adhesion to and invasion of human
   15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Major fimbrial subunit protein, type III precursor (Fimbrillin)
   78;
  periodontal tissues.
SUBCELLULAR LOCATION: Fimbria.
SIMILARITY: BELONGS TO THE P.GINGIVALIS FIMBRILLIN FAMILY.
   Nakagawa I., Amano A., Kuboniwa M., Nakamura T., Kawabata S.,
  DB 1; Length 353;
  38; Mismatches 110; Indels
  gingivalis).
Bacteroidales;
  Biochem. Biophys. Res. Commun. 197:241-247(1993).
   FUNCTION, AND CLASSIFICATION INTO TYPES
  4.7%; Score 89; 22.1%; Pred. No.
  Porphyromonas gingivalis (Bacteroides Bacteria; Bacteroides; Porphyromonadaceae; Porphyromonas.
   MEDLINE=21614934; PubMed=11748193;
  STRAIN=6/26;
MEDLINE=94071950; PubMed=7902712;
   epithelial cells.";
Infect. Immun. 70:277-285(2002).
   10 BX
353 MZ
38024 MW;
   15-JUN-2002 (Rel. 41, Created)
  EMBL; D17801; BAA04627.1; -.
   64; Conservative
  STANDARD;
  Query Match
Best Local Similarity
   11 3
353 AA;
  Fimbria; Virulence.
  SEQUENCE FROM N.A.
  (Fimbrilin).
  FMA3_PORGI
Q51826;
   SEQUENCE
   PROPEP
  69
   131
  191
  FIMA.
  106
   Matches
  q
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   염
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   Li B., Nagalla S.R., Renganathan V.; "Cellobiose dehydrogenase from Phanerochaete chrysosporium is encoded by two allelic variants."; Appl. Environ. Microbiol. 63:796-799(1997).
   -!- FUNCTION: DEGRADES BOTH LIGNIN AND CELLULOSE, OXIDIZES CELLOBIOSE TO CELLOBIONOLACTONE.
                                    246 VKGKLTKHDGTALSSEEMTAAFNAGWIVANNDPTTYYPVLVNFESNNYTYTGEAVEKGKI 305
--KEFTLHDHV----REEAQAFLRGLRVNGSQPSTF--VGVHVRRGDYVHVMPNVWKGVV 201
  Hallberg B.M., Bergfors T., Boeckbro K., Pettersson G., Henriksson G.
  Phanerochaete chrysosporium.
Wararyota; Fungi, Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Corticiaceae; Phanerochaete.
NCBI_TaxID=5306;
   CDH_PHACH STANDARD; PRT; 773 AA.

O001781, 000047;
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 41, Last annotation update)
Cellobiose dehydrogenase precursor (EC 1.1.5.1) (CDH) (Cellobiose-quinone oxidoreductase).
  quinone = cellobiono-1,5-
   -!- SUBCELLULAR LOCATION: Secreted.
  "A new scaffold for binding haem in the cytochrome domain of extracellular flavocytochrome cellobiose dehydrogenase."; Structure 8:79-88(2000).
   306 VRNHKFDINLTITGPGTNNPENPIT-----ESANLNVNCVVAAWKGV 347
   202 ADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGI 251
   ď
   Li B., Nagalia S.R., Renganathan V.; "Cloning of a cDNA encoding cellobiose dehydrogenase,
   hemoflavoenzyme from Phanerochaete chrysosporium,";
Appl. Environ, Microbiol, 62:1329-1335(1996).
   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 15-208 MEDLINE=20139694; PubMed=10673428;
  -! - CATALYTIC ACTIVITY: Cellobiose + a
   lactone + a phenol.
-!- COFACTOR: ONE FAD AND ONE HEME B.
   STRAIN=OGC101;
MEDLINE=97176414; PubMed=9023960;
  MEDLINE=97077226; PubMed=8919793;
   InterPro; IPR000172; GMC_oxred.
InterPro; IPR001100; Pyr_redox.
Pfam; PF00732; GMC_oxred; 1.
   EMBL; U46081; AAC49277.1; -. EMBL; U55888; AAB61455.1; -. EMBL; U50409; AAB92262.1; -. PDB; 127B; 18-OCT-99.
  OXIDOREDUCTASES FAMILY.
   PDB; 1D7C; 18-OCT-99.
PDB; 1D7D; 18-OCT-99.
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  CDH-1 AND CDH-2
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11;
  Query Match
4.7%; Score 89; DB 1; Length 773;
Best Local Similarity 22.0%; Pred. No. 8.5;
Matches 49; Conservative 29; Mismatches 91; Indels 54; Gaps
  238 ----NASRGDVVFAGNGIEGSPAKD-----FALLTQCNHTIMTIGTFG----IWAAYL 282
  126 GHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVRBEAQAFLRG------LRVNGSQPS 177
   178 TFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENI 237
   283 AGGDTIYLANYTLPDSPFLKVFKPEAAFLP---EWVGIPADLS 322
   499 GPTDMI----QTVQSNP-----TAAAALPPQNQWINLPVGMN 531
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Pig secretor. Sus
Rat hepatoma H35 c
Rat hepatoma H35 c
Rat hepatoma H35 c
Swine alpha(1,2) f
Swine alpha 1,2-f
   Human Sec2 catalyt
Human Sec2 protein
   Porcine secretor t
  (without alignments)
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   SIDS2/gogdata/geneseq/geneseqp-embl/AA1991.DAT:*
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SIDS2/gogdata/geneseq/geneseqp-embl/AA1992.DAT:*
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SIDS2/gogdata/geneseq/geneseqp-embl/AA1994.DAT:*
SIDS2/gogdata/geneseq/geneseqp-embl/AA1995.DAT:*
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SIDS2/gogdata/geneseq/geneseqp-embl/AA1999.DAT:*
SIDS2/gogdata/geneseq/geneseqp-embl/AA1000.DAT:*
   US-10-040-863-11
1850
1 MLVVQMPFSFPMAHFILFVF......aaflDFGWTGIAADLSPLLKH 344
  A_Geneseq_101002:*

1: /SIDS2/gggdata/geneseg/genesegp-embl/AA1980.DAT:*
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8: /SIDS2/ggdata/geneseg/genesegp-embl/AA1987.DAT:*
9: /SIDS2/gggdata/geneseg/genesegp-embl/AA1987.DAT:*
  /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
  Description
   May 27, 2003, 14:52:27 ; Search time 43.6293 Seconds
  908470
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
  Total number of hits satisfying chosen parameters:
   908470 seqs, 133250620 residues
   SUMMARIES
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   using sw model
   AAE16622
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AAW97356
AAW30630
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AAB36104
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|                                 | 112                                 | 1080.5<br>1080.5            | (U (U (U               | 4 4 4            | 365<br>365<br>365                                      | 7 1 1 2 2               | AAR13751<br>AAR80154<br>AAR70422                                                  | GDP-Fuc:beta-D-gal<br>GDP-L-fucose-beta-                                 | ta-D-gal<br>se-beta- |
|---------------------------------|-------------------------------------|-----------------------------|------------------------|------------------|--------------------------------------------------------|-------------------------|-----------------------------------------------------------------------------------|--------------------------------------------------------------------------|----------------------|
|                                 | 41.                                 | 000                         | 1 41 4                 | 4 4 4            | 365                                                    |                         | AAR70421<br>AAR70421                                                              | Z-Alpha-iu<br>Z-Alpha-fuc<br>Euman stro                                  | cosyltra<br>cosyltra |
|                                 | 16                                  | 080                         | ט וט נ                 | 44               | 300                                                    |                         | AAW23805                                                                          | Human alpha                                                              | all,2 fu             |
|                                 | 18                                  | 080                         | ) (1) (                | . 4.             | 365                                                    |                         | AAY97279                                                                          | Human Alpha<br>Human H-tra                                               | a(1,2)-r<br>ansferas |
|                                 | 20                                  | 075                         | un (u                  | п.<br>П.         | 365<br>365                                             |                         | AAW53102<br>AAY79302                                                              | Pig H trans<br>Pig alpha-1                                               | sferase.<br>1-2 fuco |
|                                 | 21                                  | 075                         | us us                  | H 0              | 365                                                    |                         | AAB47995<br>AAR45936                                                              | Swine alpha                                                              | a (1,2)              |
|                                 | 233                                 | 987                         | ) и) (                 | - <del>-</del> - | 357                                                    |                         | AAY17969                                                                          | X. laevis a                                                              | alpha-1,             |
|                                 | 25                                  | 148                         | 7                      | 0.0              | 287                                                    |                         | AAGU353U<br>AAM51992                                                              | Human secre<br>Bacteroides                                               | eted pro<br>s fragil |
|                                 | 26                                  | 144.5                       |                        | α α              | 300                                                    |                         | AAY92713                                                                          | H. pylori L                                                              | UA802 al             |
|                                 | 28                                  | 100                         |                        | 9 401            | 322                                                    |                         | AAY70408                                                                          | neilcobacie<br>C. elegans                                                | alpha-1              |
|                                 | 30.0                                | 92                          |                        | <u>ه</u> .       | 575                                                    |                         | AAW22124<br>ABG34136                                                              | Pig alpha l<br>Antibody py                                               | 1-6 fuco             |
|                                 | 31                                  | 90.5                        |                        | · .              | 661                                                    |                         | AAU39722                                                                          | Propionibac                                                              | cterium              |
|                                 | 3 3<br>3 3<br>3 3                   | 000                         |                        | ຫຸ ຫຼ            | 515                                                    |                         | AAG73884<br>AAR15057                                                              | Human color                                                              | n cancer             |
|                                 | 34                                  | 000                         |                        | <br>. o          | 575                                                    |                         | AAW22125                                                                          | Eliman alpha                                                             | 7420C23              |
|                                 | 35                                  | 060                         |                        | 0,0              | 575                                                    |                         | ABB08405                                                                          | Alphal, 6-fu                                                             | ucosyl t             |
|                                 | 36                                  | 000                         |                        | o, o             | 1073                                                   |                         | ABG28599                                                                          | Novel humar                                                              | n diagno             |
|                                 | , a<br>a<br>a                       | 87.5                        |                        | ۰۲.              | 365                                                    |                         | AAM/9361<br>AAW80571                                                              | Human prote<br>Human heart                                               | ein SEQ<br>F O-fuco  |
|                                 | 99                                  | 87.5                        |                        | .7               | 397                                                    |                         | AAW80573                                                                          | Human O-fuc                                                              | cosyltra             |
|                                 | 40                                  | 87                          |                        | ۲.               | 637                                                    |                         | ABB71200                                                                          | Drosophila                                                               | melanog              |
|                                 | 42                                  | 86.5                        |                        |                  | 958                                                    |                         | AAY51120                                                                          | Human prote                                                              | ein SEQ<br>-2 prote  |
|                                 | 43                                  | 85.1                        |                        | 9.               | 547                                                    |                         | ABG24778                                                                          | Novel human                                                              | diagno               |
|                                 | 44                                  | 85.5<br>85                  |                        | ب ب              | 739                                                    |                         | AAG93019<br>ABB63790                                                              | tami<br>phil                                                             | _ =                  |
|                                 |                                     |                             |                        |                  |                                                        |                         | ALIGNMENTS                                                                        |                                                                          |                      |
| RESU                            | ILT 1                               |                             |                        |                  |                                                        |                         |                                                                                   |                                                                          |                      |
| AAB3                            | AAB3                                | 9019                        | standar                | ď,               | Protein                                                | n; 3                    | 144 AA.                                                                           |                                                                          |                      |
| A X                             | AAB3                                | 36106;                      |                        |                  |                                                        |                         |                                                                                   |                                                                          |                      |
| X                               | 19-                                 | EB-20                       | 01 (                   | first            | entry                                                  | 0                       |                                                                                   |                                                                          |                      |
| XX<br>CE<br>XX                  | Human                               | n Sec                       | ~                      | catalvtic        | n domain                                               | ٠.<br>ت                 |                                                                                   |                                                                          |                      |
| ×                               |                                     | )                           | ,                      | 4                |                                                        |                         |                                                                                   |                                                                          |                      |
| KW Huma KW neur KW immu KW smal | Human;<br>neurop<br>immuno<br>small | n;<br>oppi<br>not           | 2;<br>cti<br>apy<br>lu | cd ** *d         | phal-2fucos<br>nootropic;<br>mmunosuppre<br>carcinoma. | osyl<br>c, g<br>ress    | -2fucosyltransferase;<br>tropic; gene therapy;<br>osuppression; cancer;<br>inoma. | cytostatic;<br>Fucalphal-2Galbetal-3GalNAc<br>neurological disease;      | NAc;                 |
| SO                              | Ното                                | sapi                        | ens.                   |                  |                                                        |                         |                                                                                   |                                                                          |                      |
| N N                             | WOZ                                 | 00644                       | 64-A1                  |                  |                                                        |                         | 1                                                                                 |                                                                          |                      |
| X G                             | 02-1                                | -NOV-2000                   | .00                    |                  |                                                        |                         |                                                                                   |                                                                          |                      |
| PF                              | 23-                                 | 2R-19                       | :65                    | -0M66            | 9WO-US0738                                             | 84.                     |                                                                                   |                                                                          |                      |
| X K                             | 23-1                                | PR-19                       | 66;                    | -0M66            | -08073                                                 | 94.                     |                                                                                   |                                                                          |                      |
| PA                              | (PACI                               | (-I                         | PACIFI(                | C NORT           | NORTHWEST                                              | CANCER                  | CER FOUND.                                                                        |                                                                          |                      |
| XX<br>Id                        | Holmes                              | nes EH,                     | , She                  | erwood           | AL;                                                    |                         |                                                                                   |                                                                          |                      |
| X X<br>DR                       | WPI                                 | 2000                        | -68726                 | 62/67.           |                                                        |                         |                                                                                   |                                                                          |                      |
| X                               |                                     | 1                           | ,-                     |                  | 7                                                      |                         | -                                                                                 |                                                                          | 1                    |
| PT                              | pre                                 | new rat gang<br>preparation | of<br>of               | oside GMI.       | GM1"s<br>syl GM                                        | 4-specific<br>GM1 which | alp<br>is                                                                         | phal-ZFucosyltransferase, useful for useful as a nutritional composition | l for<br>ition       |

```
AAW37855;
   Sednence
   Query Match
                   (KELL/)
(LENN/)
(LOWE/)
  (ROUQ/)
         (GIOR/)
   300 (
   301
  121
  121
   181
  RESULT 3
  AAW37855
  ŏ
   QQ
   QY
   ÖΫ
  Dp
  g
  δŏ
  g
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  q
δŏ
   The present sequence is given in a specification relating to a rat
ganglioside GM 1-specific alphal-2fucosyltransferase protein. The protein
c ganglioside GM 1-specific alphal-2fucosyltransferase protein. The protein
c rits cellular fraction is useful for synthesis of a molecule comprising
c rucalphal-2calbetal-3GalNAc.
c rucalphal-2calbetal-3GalNAc a glycolipid, glycoprotein, glycolipoprotein
c or a free oligosaccharide comprising Fucalphal-2GalDetal-3GalNAc.
c and a molecule or glycolipid, glycoprotein, glycolipoprotein or
c oligosaccharide having a terminal Galbetal-3GalNAc group. It is also
c oligosaccharide having a terminal Galbetal-3GalNAc group. It is also
c oligosaccharins, glycolipids and oligosaccharides are useful as
glycolipoproteins, glycolipids and oligosaccharides are useful as
c nutritional compositions and fucosyl-GM_1 is useful for inducing an
c immunotherapeutic or immunosuppressive action against cancer,
c neurological disease or small cell iung carcinoma.
   ;
0
   Sec2; alpha(1,2) fucosyltransferase; H blood group; secretor genotyping; GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase; human; FUT2; nonsecretor genotyping.
  240
  VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT 300
   RIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ 180
   120
   9
   0; Gaps
  181 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF
   61 RGMWIINAIGRLGNQMGEXATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS
   1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL
  Score 1850; DB 21; Length 344; Pred. No. 2.5e-186;
   or immunotherapeutic for cancer and neurological diseases
  Indels
   GGDIIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  ;
0
  Query Match
Best Local Similarity 100.0%; Pred. No. 2.5
Matches 344; Conservative 0; Mismatches
   AAW69332 standard; Protein; 343 AA
                           Example; Fig 3B; 91pp; English.
  95US-0395800.
   Human Sec2 protein sequence.
  95US-0395800
   (first entry)
  344 AA;
  28-FEB-1995;
   Homo sapiens
   28-FEB-1995;
  20-NOV-1998
   US5807732-A
   15-SEP-1998
  AAW69332;
   Sequence
   241
  301
  301
  121
  RESULT 2
  AAW69332
   g
   qq
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  δŽ
  Db
   Dò
  δŽ
  qq
  g
  QΫ́
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This sequence is the human Sec2 protein of the invention. The DNA encodes a alpha(1,2) fucosyltransferase and is the Secretor alpha(1,2)fucosyltransferase locus, that cross hybridises with the H blood group alpha(1,2)fucosyltransferase gene. The DNA is useful for producing a recombinant human GDP-L-fucose.beta-D-galactoside 2-alpha-L-fucosyltransferase (FUT2) which can be used for genotyping an individual as a secretor or nonsecretor as it is known that nonsecretors homozygous for a mutant allele of the FUT2 gene that has a stop codon in the position corresponding to amino acid 143.
  241 VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWANLT 300
  RIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ 180
   61 RGMWTINAIGRLGNOMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120
  1 MLVVQMPFSFPMAHFILEVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL 60
   Gaps
  DNA encoding fucosyltransferase enzyme - useful for producing recombinant enzyme and genotyping person as secretor or nonsecretor
  KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF
  ή;
  DB 19; Length 343;
   Secretor; glycosyltransferase; FUI2; pig; epitope; antigen;
transgenic animal; xenotransplantation; organ transplant.
   0; Indels
  GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  Rouguier
  Score 1832.5; DB 1
Pred. No. 1.8e-184;
  0; Mismatches
  Lennon G, Lowe JB,
  Disclosure; Column 45-50; 55pp; English.
   Porcine secretor transferase (FUT2)
  AA
  AAW37855 standard; Protein; 340
   99.18;
  (first entry)
   Best Local Similarity 99./
Matches 343; Conservative
  Giorgi D, Kelly RJ,
   WPI; 1998-520127/44.
N-PSDB; AAV58323.
GIORGI D.
KELLY R J.
LENNON G.
LOWE J B.
ROUQUIER S.
   Similarity
  343 AA;
  28-AUG-1998
  Sus scrofa
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KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF

181

us-10-040-863-11.rag

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5
  This polypeptide comprises porcine secretor glycosyltransferase (SE or FUT2), a type II integral membrane protein has high affinity of the type I and type III substrates. Its amino acid sequence was deduced from the nucleotide sequence of a genomic DNA clone (see AAV29003) isolated from a pigl liver library on the basis of homology to human FUT2 cDNA. Pig FUT2 shows 83.2% identity with human FUT2. Expression of a glycosyltransferase, such as porcine Se, in a tissue results in reduced expression of unwanted carbohydrate epitopes on the tissue, especially porcine heart, liver, kidney or copitopes on the tissue, especially porcine heart, liver, kidney or epitopes on the tissue, especially porcine heart, liver, kidney or copitopes on the tissue, especially porcine seart, liver, kidney or immunogenic and of increased immunological acceptablity. A claimed method of producing a cell from a donor species that is immunologically acceptable to a recipient species involves reducing levels of carbohydrate on the donor cell that causes it to be recognised as non-self by the recipient by expressing a nucleic acid for a glycosyltransferase such as porcine Se in the cell.
   RGMWIINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRIILPVLHSATAS 120
   Gaps
   MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL 60
  RIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ
  Nucleic acid encoding glycosyltransferase able to compete with second such enzyme - particularly used to reduce expression of unwanted carbohydrate epitope(s) on tissues intended for
  Length 340;
   Indels
                                /note= "N-terminal cytoplasmic tail"
  82.6%; Score 1528; DB 19;
82.0%; Pred. No. 2.3e-152;
ive 24; Mismatches 34;
  251..253
/note= "Asn is N-glycosylated"
279..281
/note= "Asn is N-glycosylated"
305..307
  /note= "C-terminal domain"
185..187
/note= "Asn is N-glycosylated"
  /note= "Asn is N-glycosylated"
   'note= "transmembrane domain'
Location/Qualifiers
   Claim 6; Fig 1A-B; 40pp; English.
  97WO-AU00540
   96AU-0001823
   McKenzie IFC, Sandrin MS;
   282; Conservative
   27..340
  (AUST-) AUSTIN RES INST.
  WPI; 1998-169148/15.
   Similarity
   340 AA;
   N-PSDB; AAV29003
  transplantation
   Modified-site
   Modified-site
   Modified-site
   Modified-site
   WO9807837-A1
  22-AUG-1997;
   23-AUG-1996;
   26-FEB-1998
   Sequence
  Query Match
   Local
  Domain
   Domain
                  Domain
   Matches
  58
   121
   g
   Dp
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The present sequence represents pig secretor used in an example of the present invention. The present invention describes nucleic acids (NA) encoding a chimeric glycosyltransferase. The NAs comprise a catalytic domain of a first glycosyltransferase (GT) and a localisation signal of a second GT, whereby when the NA is expressed in a cell and where the chimeric enzyme is located in an area of the cell where it is able to compete for substrate with a second GT, resulting in reduced levels of a product from the second GT. The NAs can be used to produce cells and organs with desired glycosylation patterns. Products and methods of the present invention can be used to reduce the levels of undesirable
Gaps
  Nucleic acids encoding chimeric glycosyltransferases - used for altering carbohydrate levels on the surface of cells, useful in gene therapy and transplantation
  1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQİPVLASTSKALGPSQL 60
  VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT
  4;
  Length 340;
  Pig; secretor; chimeric; glycosyltransferase; gene therapy;
   Indels
   301 GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
   34;
  82.6%; Score 1528; DB 19;
82.0%; Pred. No. 2.3e-152;
ive 24; Mismatches 34;
   Example 2; Fig 6; 51pp; English.
  transplantation or gene therapy.
   AAW53101 standard; Protein; 340
  96US-0024279.
96AU-0001402.
   97WO-AUG0492.
  (first entry)
   Sandrin MS;
   Best_Local Similarity 82.09
Matches 282; Conservative
  (AUST-) AUSTIN RES INST.
  WPI; 1998-159170/14.
   340 AA;
   N-PSDB; AAV21639
   transplantation.
  McKenzie IFC,
   01-AUG-1997;
  Pig secretor
  WO9805768-A1
   21-AUG-1996;
   02-AUG-1996;
  08-JUL-1998
  12-FEB-1998.
   Sus scrofa.
   AAW53101;
  Sequence
   Query Match
           177
   241
  RESULT 4
           g
  δŽ
  g
  ŏ
   Dp
   δλ
   qq
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  a
  ōλ
   g
  ŏ
   Db
   Q_{\overline{Y}}
   g
   Ω
  qq
   The present sequence was given in a specification relating to an isolated rat ganglioside GM_repecific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-2Galbetal-3GalRAC, a glycolipid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising rucalphal-2Galbac. The method involves contacting alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoprotein, glycolipoprotein or oligosaccharide having a terminal by contacting the protein with GDP-fucose and ganglioside GM_1 The obtained glycoproteins, glycolipoproteins, glycolipids and oligosaccharides are useful as nutritional compositions and fucosyl-GM_1
  New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
   is useful for inducing an immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
RGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120
                       117
   180
  176
  240
  300
  Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2calbetal-3calNAc; immunotherapy; fimnuosuppression; cancer; neurological disease; small cell lung cancinoma
           VVTSNGMAWCRENIDISHGDVVFAGDGIEGSPAKDFALLTQCNHIIMIGTEGIWAAYLT
   RIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ
   KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF
  GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  H35 cell alphal-2fucosyltransferase.
   (PACI-) PACIFIC NORTHWEST CANCER FOUND.
  AAB36104 standard; Protein; 380 AA
   Claim 1; Fig 5; 91pp; English
   99WO-US07384.
  99WO-US07384
   (first entry)
  Holmes EH, Sherwood AL;
  WPI; 2000-687262/67.
N-PSDB; AAC67965.
   Rattus norvegicus
   WO200064464-A1
   Rat hepatoma
   23-APR-1999;
  23-APR-1999;
   19-FEB-2001
   02-NOV-2000
   AAB36104;
 61
  181
   121
  118
  177
  241
  301
   297
   RESULT 5
  ŏ
  qq
  Db
   ŎΫ
  g
                   g
  ^{\circ}
   qq
   QΥ
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'n
  109
  Rat; alphal-2fucosyltransferase; alphal-2FucT; antisense therapy; galactose betal-3N-acetylgalactosamine; Galbetal-3GalNac; glycolipid; glycoprotein; glycolipoprotein; oligosaccharide; fucosyl-GMI; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GMI; cell transformation
  9
  Gaps
  MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAM--WELPV-----QIPVLA 49
   SLPVLHSDTAKKIPWQNYHLNDWMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEF
   STSKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI
   110 TLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEF
  TLHDHVREEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALD
  230 WFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTI
   240 MFRARYSSPVEVVTSNGMAWCRENINASRGDVVFAGGNGIEGSPAKDFALLTQCNHTIMII
  12;
                                      380;
  GTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLK
  /note= "Intracellular/Transmembrane domain"
                                      Length
  Indels
   /note= "Region which overlaps rat
                                    Score 1475; DB 21;
Pred. No. 1.1e-146;
  Mismatches
   'note= "N-glycosylated"
   /note= "N-glycosylated"
  293
/note= "N-glycosylated"
  Location/Qualifiers
  AAE16622 standard; Protein; 380 AA
   Rat hepatoma H35 cell alphal-2FucT
  30;
                                  79.78;
77.78;
  99US-029886
  (NWHO-) NORTHWEST HOSPITAL
   (first entry)
  Conservative
  221..380
   Sherwood AL;
  661
   Similarity
380 AA;
  Rattus norvegicus.
  Modified-site
  Modified-site
  Modified-site
   JS6329170-B1
  23-APR-1999;
   09-APR-2002
  11-DEC-2001
   Holmes EH,
   AAE16622;
Sequence
                                  Query Match
   Domain
  Region
  170
   290
   20
   61
   121
  Matches
  9
   AAE16622
  RESULT
```

99WO-US07384

WO200064464-A1

02-NOV-2000

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Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease;
   Rat hepatoma H35 cell alphal-2fucosyltransferase catalytic domain.
   AAB36105 standard; Protein; 353 AA
  19-FEB-2001 (first entry)
   WPI; 2002-121132/16.
N-PSDB; AAD27207.
   alphal-2FucT.
   AAB36105;
  Seguence
   Query Match
  230
   50
   121
   180
  300
  61
  290
   RESULT 7
   AAB36105
QY
  Db
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small cell lung carcinoma.

Rattus norvegicus

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(PACI-) PACIFIC NORTHWEST CANCER FOUND.
   Holmes EH, Sherwood AL;
   WPI; 2000-687262/67.
N-PSDB; AAC67966.
  23-APR-1999;
ŏ
  Db
   ά
   g
  δ
   3,
   (alphal-ZFucT) engages of late out sort specialist alphal-Zenocyticiansterase (alphal-ZFucT) engyme and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate moiety found in ganglisoside GM1, at terminal galactose betal-3N-acetylgalactosamine (Galbetal-3GalNAc) saccharide. Alphal-ZFucT DNA is useful for producing rat alphal-ZFucT DNA is useful for producing rat alphal-ZFucT protein by recombinant techniques. Alphal-ZFucT DNA is useful for the preparative synthesis of fucosyl containing glycolipids, glycoproteins, glycolipoproteins and oligosaccharide, and for preparing fucosyl-GM1. Alphal-ZFucT DNA is useful for detecting oncogenic transformation which alphal-ZFucT is activated in cell transformation, antisense sequences derived from alphal-ZFucT DNA are useful for inhibiting, suppressing or treating cancer. Alphal-ZFucT DNA is useful in gene therapy and mitisense therapy and antisense therapy. The present sequence is rat hepatoma H35 cell
   Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for producing GMI-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues
  STSKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI 109
  169
   239
   1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAM--WELPV-----QIPVLA 49
   Gaps
  The invention relates to rat GM1-specific alpha1-2fucosyltransferase
   110 TLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEXVRFTGYPCSWTFYHHLRQEILQEF
   170 TLHDHVREEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALD
  WFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTI
  12;
  79.7%; Score 1475; DB 23; Length 380; 77.7%; Pred. No. 1.1e-146; Live 30; Mismatches 37; Indels 12
  Claim 3; Fig 5; 41pp; English.
  Best Local Similarity 77.7 Matches 275; Conservative
  380 AA;
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ganglioside GM_1-specific alphal-2 fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-12 Galbetal-3 fallNac, a glycollpid, glycolotein, glycolipoprotein, or a free oligosaccharide comprising Fucalphal-2 Galbetal-3 GalNac. The method involves contacting aphal-2 fucosyltransferase with SDF-1 and a molecule or glycolipid, glycorotein, glycolipoprotein or oligosaccharide having a terminal Galbetal-3 GalNac. It is also useful for synthesis of fucosyl-GM_1 by contacting the protein with GDF-fucose and ganglioside GM_1. The obtained glycoproteins, glycolipids and oligosaccharides are useful as nutritional compositions and fucosyl-GM_1 is useful for inducing an immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
  m
New rat ganglioside GMI-specific alphal-2Pucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
   196
  GEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLNDWMEEE 136
   12; Gaps
  28 VQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGMWTINAIGRLGNQM 76
  The present sequence is given in a specification relating to a rat
   VGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDT
   SHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSP
   YRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRGLQVNGSRPGTF
  Length 353;
   Indels
  ---
   74.4%; Score 1376; DB 21;
78.9%; Pred. No. 2.7e-136;
live 26; Mismatches 31;
   FLKVFKPEAAFLPEWVGIPADLSPLLK 326
  AAE16623 standard; Protein; 353 AA.
  Claim 2; Fig 3A; 91pp; English.
   258; Conservative
   Best Local Similarity
  353 AA;
  Seguence
   AAE16623;
  Query Match
   240
   Matches
   77
   137
   197
  300
   317
  RESULT 8
  AAE16623
   g
  d
   δ
  Qγ
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WPI; 2002-121132/16.
N-PSDB; AAD27208.
                              Rattus norvegicus.
                                    Key
Modified-site
   Modified-site
   Modified-site
   Modified-site
        Rat hepatoma
   US6329170-B1
  23-APR-1999;
  23-APR-1999;
  09-APR-2002
  11-DEC-2001
  Seguence
   Query Match
  Region
```

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Swine alpha(1,2)fucosyltransferase, FUT1, Escherichia coli, resistant, E. coli-associated intestinal disorder, E coli infection.
   The present sequence represents swine alpha(1,2) fucosyltransferase (FUT1). The specificatino describes methods relating to Escherichia coli-resistant swine. One of the methods for identifying a swine resistant to E. coli-associated intestinal disorders, comprises determining whether the base at 307 of alpha(1,2) fucosyltransferasel gene (FUT1) is adenine (sic), in which case the swine are resistant. The porcine FUT1 polymorphisms can be used to develop drugs for the treatment of swine having E. coli-associated disease. The methods can also be used in breeding programmes to identify swine with resistance
SHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLFGGDTIYLANYTLPDSP 316
   240 SRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSP 299
  YRHIPPGEYVRFTGYPCSWIFYHHLRQEILQEFTLHDHVREEAQKFLRGLQVNGSRPGTF
   VGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDT
  58.5%; Score 1081.5; DB 20; Length 365; 65.5%; Pred. No. 3.3e-105; ive 30; Mismatches 66; Indels 11;
   Identifying swine genetically resistant to E. coli associated diseases ~ using PCR-RFLP to assay for polymorphisms in the alpha(1,2) fucosyltransferase 1 gene
  (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
  FLKIFKPEAAFLPEWTGIAADLSPLLK 343
  Swine alpha(1,2) fucosyltransferase.
  AA
   Disclosure; Fig 1; 19pp; English.
   AAW97356 standard; Protein; 365
  98WO-US10259
  97US-0047181
  Query Match
Best Local Similarity 65.5
Matches 203; Conservative
  WPI; 1999-131692/11.
N-PSDB; AAX15872.
  to E coli infection
   365 AA;
   WO9853101-A2
  20-MAY-1998;
  20-MAY-1997;
  Bosworth BT;
  13-MAY-1999
   26-NOV-1998
  Synthetic.
  AAW97356;
   Seguence
   ds sns
                    61
   121
  257
  317
   137
  RESULT 9
   . 유
   QΣ
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   gg
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   gg
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  contained year-cose Decentained Contained (Galbell-Stanke) accordanted. Alphal-2FucT DNA is useful for producing rat alphal-2FucT DNA is useful for producing rat alphal-2FucT protein by recombinant techniques. Alphal-2FucT DNA is useful for the preparative synthesis of fucosyl containing divocipieds, glycoproteins, glycolipoproteins and oligosaccharide, and for preparing fucosyl-GAL. Alphal-2FucT DNA is useful for detecting oncogenic transformation which alphal-2FucT DNA is useful for detecting oncogenic transformation which alphal-2FucT is activated in cell transformation, antisense sequences derived from alphal-2FucT DNA are useful for inhibiting, suppressing antisense therapy. The present sequence is rat hepatoma H35 cell alphal-2FucT catalytic domain.
  (alphal-2Fucr) enzyme and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate moiety found in ganglioside GM1, a terminal galactose betal-3N-acetylgalactosamine (Galbetal-3GalNAc)
  Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for producing GMI-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues .
   Rat; alphal-2fucosyltransferase; alphal-2FucT; antisense therapy; galactose betal-3N-acetylgalactosamine; Galbetal-3GalNAc; glycolipid; glycoprotein; glycolipoprotein; oligosaccharide; fucosyl-GMI; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GMI;
  invention relates to rat GM1-specific alphal-2fucosyltransferase
  28 VQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGMWTINAIGRLGNQM 76
  Length 353;
  Indels
  H35 cell alphal-2FucT catalytic domain.
   74.4%; Score 1376; DB 23; 1arity 78.9%; Pred. No. 2.7e-136; Conservative 26; Mismatches 31;
  'note= "N-glycosylated"
  /note= "N-glycosylated"
  'note= "N-glycosylated"
  'note= "N-glycosylated"
  transformation; catalytic domain.
   Location/Qualifiers
  Claim 4; Fig 3; 41pp; English
   99US-0298886
   99US-0298886
                (first entry)
   (NWHO-) NORTHWEST HOSPITAL
   Holmes EH, Sherwood AL;
  Similarity
   353 AA;
  Local Simi
les 258;
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11; Gaps

77 GEYATLXALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLNDWMEEE 136

Matches

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   A method has been developed for the identification of swine that are resistant to intestinal colonisation by E. coli. The method comprises determining whether a genetic polymorphism associated with resistance to colonisation is present in a swine sample, and then inferring that the swine is resistant if it is homozygues for the polymorphism. The method uses the swine alpha-1,2-fucosyltransferase (FUT1) polymorphism. The present sequence represents swine FUT1. The method enables the breeding
                             51 PVAIFCLAGTPVHPNASDSCPKHPASFSGTWTIYPDGREGNOMGOYATLLALAQLNGRQA 110
  229
   PAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSFFLKIFKPEAAFLPEW 331
   PVQIPVLAST-----SKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPA
  94 FIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPC
   SWIFYHHLRQEILQEFTLHDHVREEAQKFLRGLQV--NGSRPGTFVGVHVRRGDYVHVMP
   KVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGS
  New method of identifying swine that are resistant to intestinal colonisation by Escherichia coli - comprises use of genetic polyworphic markers, used for breading swine resistant to Escherichia coli-related diseases
  Swine, pig; alpha-1,2-fucosyltransferase 1; FUT1; resistance; Escherichia coli; infection; oedema; postweaning diarrhoea; intestinal disorder; polymorphism.
   Swine alpha-1,2-fucosyltransferase 1 protein.
  (SWTE-) SWISS FEDERAL INST TECHNOLOGY ZURICH. (USDA ) US SEC OF AGRIC.
   & DEV CORP
  AAW30630 standard; Protein; 365 AA.
  Example 6; Fig 1; 35pp; English
  98WO-US10318
   97US-0047181
  (first entry)
  (BIOT-) BIOTECHNOLOGY RES
   Vogeli P;
   350 VGINADLSPL 359
   TGIAADLSPL 341
  WPI; 1999-059746/05.
   N-PSDB: AAX03811
   Bosworth BT,
  20-MAY-1998;
  01-APR-1999
   20-MAY-1997;
  W09853102-A1
   26-NOV-1998.
   Sus scrofa.
   AAW30630;
   212
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   154
  170
   AAW30630
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of swine that are resistant to E. coli-related diseases. This method gene. Wore particularly, the agenctic polymorphism in the FUTI gene. Wore particularly, the alentification method identifies swine that are resistant to E. coli-related intestinal disorders if, in a sample taken, the only nitrogen base at residue 307 in the FUTI gene is adenine. Larger amplified fragments from the assay can be used for RELP analysis, and the assay itself is used as a basis for a kit, applied to swine of arganger. The polymorphisms associated with E. coli FHB or receptors. The polymorphisms associated with E. coli fills swine with E. coli-related diseases. However, a mutated form of the from producing the intestinal recentor for FIR was and prevent it from producing the intestinal recentor for FIR was and prevent it
   from producing the intestinal receptor for F18. The detection of polymorphic markers in the method disclosed enables the detection and treatment of E. coli-related intestinal diseases in swine, where there
   has been no success using antibiotics due to unsuccessful prophylaxis
  51 PVAIFCLAGTPVHPNASDSCPKHPASFSGTWTIYPDGRFGNOMGQYATLLALAQLNGRQA 110
  211
  FIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPC 153
   271
   331
   42 PVQIPVLAST-----SKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPA 93
   272 PAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEW
   11 FIQPAMHAVLAPVFRITLPVLAPEVDRHAPWRELELHDWMSEDYAHLKE-PWLKLIGFPC
   212 KVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDG1EGS
  SWTFYHHLRQEILQEFTLHDHVREEAQKFLRGLQV--NGSRPGTFVGVHVRRCDYVHVMP
   58.5%; Score 1081.5; DB 20; Length 365; 65.5%; Pred. No. 3.3e-105; 1ve 30; Mismatches 66; Indels 11;
   GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase.
  AA.
  AAR13751 standard; Protein; 365
   90US-0627621
  90US-0479858
  91WO-US00899
   90US-0480133
  (first entry)
  Best Lccal Similarity 65.5
Matches 203; Conservative
   OF MICHIGAN.
  350 VGINADLSPL 359
   332 TGIAADLSPL 341
  Glycosyltransferase
  365 AA;
  Homo sapiens
  AIND ( IMNA)
  07-NOV-1991
  14-FEB-1991;
   12-DEC-1990;
  WO9112340-A.
   22-AUG-1991,
   14-FEB-1990;
   Seguence
   Query Match
   AAR13751;
  94
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LHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD 173
  ALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV 113
  Gaps
  MAHFILEVFTVSTIFHVQQR-----ASTSK 53
  The amino acid sequence codes for a protein capable of functioning as a GDP- Fuc: Deta-D-Gal alpha(1.2)- fucosyltransferase. The functional protein is represented by amino acids 33 to 365. The enzyme produced by the DNA sequence can be used in enzymatic fucosylation of feath-terminating galactose residues on lactosemente or neolacto type beta-D-galactoside to alpha-2-L-fucose residues. See also AAR13749-R13752.
   GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase; Fuc-T; synthesis; 2'-fucosyllactose; oligosaccharide; human milk; non-human transgenic mammal; secondary gene product.
   RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGT
   HVREEAQKFLRGLQV --NGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWF
   GDP-L-fucose-beta-D-galactosidase alpha-1,2-fucosyltransferase.
  21;
   DB 12; Length 365;
   Isolation of gene conveying post-translational characteristic e.g. the presence of soluble or membrane bound oligo or polysaccharide or glycosyltransferase.
  79; Indels
   58.4%; Score 1080.5; DB 1.
59.7%; Pred. No. 4.2e-105;
tive 41; Mismatches 79;
  AA.
  English.
  AAR80154 standard; Protein; 365
   94US-0209122.
  Disclosure; Fig 3; 155pp;
   (first entry)
  Conservative
                   WPI; 1991-267151/36.
P-PSDB; AAR13751.
  Similarity
  365 AA;
   24-JAN-1995;
   09-MAR-1994;
  Homo sapiens
   WO9524494-Al
   25-JUN-1996
   209;
  14-SEP-1995
  Sequence
  Query Match
Best Local 9
Lowe JB;
  AAR80154;
   Best Loca
Matches
  174
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   114
   71
   131
   190
   RESULT 1
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is encoded by CDNA (AAQ99461) isolated from a human epidermal carcinome cell line. The enzyme is responsible for the synthesis of 2'-fucosylactose, one of the oligosaccharides in human milk. Other products of Fuc-T include glycoprotiens contq. beta-linked terminal galactose residues which can be fucosylated by Fuc-T. This DNA can be used to produce non-human transgenic mammals able to produce secondary gene products, e.g. oligosaccharides, in their milk. The transgenic mammals milk biochemically resembles human milk. This humanised milk can be used in the prepn. of an enteral nutritional product useful in the nutritive maintenance of an animal.
   54 ALGPSQLRGMWIINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV 113
   173
   231
   21; Gaps
  ---LAKIQAMWELPVQIPVL-----ASTSK 53
  Prodn. of human:ised milk by non-human transgenic mammal - by inserting heterologous gene encoding human catalytic entity which produces oligo:saccharide(s) and glyco:conjugate(s) into mammal's
   GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase; glycosyltransferase; glycosylation; oligosaccharide; glycoprotein; glycolipid; transgenic animal; cattle; milk.
   LHSATASRIPWQNYHLNDWMEBEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD
   HVREEAQKFLRGLQV - - NGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWF
  RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGT
  58.4%; Score 1080.5; DB 16; Length 365; 59.7%; Pred. No. 4.2e-105;
   GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase
  FGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPL 341
   79; Indels
  Mukerji P;
  41; Mismatches
  C, Moreman KW,
Smith DF;
   Example 1; Page 62-64; 83pp; English.
  12 MAHFILFVFTVSTIFHVQQR-----
  AAR70422 standard; Protein; 365
  2-Alpha-fucosyltransferase.
   Kopchik JJ,
  Conservative
  Prieto PA,
  WPI; 1995-336739/43.
  (first
               (ABBO ) ABBOTT LAB
   Best_Local Similarity
Matches 209; Conserv
   365 AA;
   N-PSDB; AAQ98461
  Cummings RD,
  27-FEB-1996
  Pierce JM,
   Sequence
  Query Match
  AAR70422
  genome
  232
  RESULT 13
  AAR70422
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Human H-transferase
  Cummings
  Seguence
   Query Match
  AAR90572;
   310
  232
  RESULT 15
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  XEXEXEX
  4;
  54 ALGPSQLRGMWTINAIGRLGNOMGEYATLYALAXMNGRPAFIPAQMHSTLAPIFRITLPV 113
  114 LHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD 173
  231
   New transgenic non-human mammal milk prods - contg. heterologous components produced as secondary gene prods. of an heterologous gene
  Gaps
   12 MAHFILFVFTVSTIFHVQQR------LAKIQAMWELPVQLPVL------ASTSK 53
  11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
   2-Alpha-fucosyltransferase (AAR70422) is encoded by a cDNA clone (AAR701083) isolated from a human epidermal carcinoma A431 library. The enzyme can be expressed in the milk of a transgenic mammal, esp. cow. This allows large-scale prodn. of oligosaccharides and glycosylated proteins and lipids in the milk.
   HVREEAQKFLRGLQV -- NGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWF
  RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGT
   58.4%; Score 1080.5; DB 16; Length 365; 59.7%; Pred. No. 4.2e-105; Live 41; Mismatches 79; Indels 21;
  21;
  GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase; glycosyltransferase; oligosaccharide; glycoprotein; glycolipid; transgenic animal; cattle; glycosylation; milk.
  FGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPL 341
  Mukerji
   JJ, Moremen KW,
Smith DF;
  Example 1; Page 62-64; 83pp; English.
   AA.
  Protein; 365
   95WO-US00967
   94US-0208889
   2-Alpha-fucosyltransferase.
   (first entry)
   Local Similarity 59.7 hes 209; Conservative
  , Kopchik Prieto PA,
   WPI; 1995-328284/42.
N-PSDB; AAT01083.
   ABBO ) ABBOTT LAB
   AAR70421 standard;
  365 AA;
Homo sapiens
   24-JAN-1995;
   09-MAR-1994;
  Cummings RD,
                 W09524495-A1
   27-FEB-1996
                                     14-SEP-1995
   Pierce JM,
   Seguence
   AAR70421;
   Query Match
   Best Loca
Matches
   131
   232
   292
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   250
   RESULT 14
  AAR70421
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54 ALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV 113
   189
  114 LHSATASRIPWONYHLNDWMEEEYRHIPPGEXVRFTGYPCSWTFYHHLRQEILQEFTLHD 173
  RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMFIGT 291
   53
   11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
   Alpha-1,2-fucosyltransferase (AAR70421) is encoded by a cDNA clone (AAT01082) isolated from a human epidermal carcinoma cell line A431 cDNA library. The enzyme can be expressed in the milk of a transgenic mammal, esp. cow. This allows large-scale prodn oligosaccharides or glycosylated proteins and lipids in the milk.
  12 MAHFILFVFTVSTIFHVQQR------LAKIQAMWELPVQIPVL-----ASTSK
   174 HVREEAQKFIRGLQV--NGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDW?
   DB 16; Length 365;
   metabolite prodn esp. glycosyltransferase for prodn. of oligosaccharide(s) and glyco-conjugate(s) in the milk, useful foods, pharmaceuticals, etc.
   - used in
  FGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPL 341
   Indels
  Transgenic animal expressing heterologous catalyst
   ь,
Б
   58.4%; Score 1080.5; DB 1659.7%; Pred. No. 4.2e-105;
  Mukerji
  41; Mismatches

    Moremen KW,
Smith DF;

   Example 1; Page 62-64; 84pp; English.
   AA.
   95WO-US01147
  94US-0209132
  AAR90572 standard; Protein;
  Kopchik JJ,
  Best Local Similarity 59.79
Matches 209; Conservative
   Prieto PA,
  WPI; 1995-328279/42.
N-PSDB; AAT01082.
   (ABBO ) ABBOTT LAB
   365 AA;
Homo sapiens
  WO9524488-A1
  24-JAN-1995;
   09-MAR-1994;
  RD,
   14-SEP-1995
  08-APR-1996
  Pierce JM,
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Page 10

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4;
  The human H-transferase (AAR90572) product of a cDNA clone (AAT12238) prepd. from human epidermoid carcinoma cells (ATCC CRL 155 A-431) can be expressed in xenogenetic organs, tissues and cells using a vector such as papex-1 (AAT12239). This results in decreased expression of the non-human antigen galactose alpha(1,3) galactose on the surface of the organs etc. so that hyperacute rejection is reduced upon transplantation to humans.
  54 ALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV 113
   114 LHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD 173
  HVREEAQKFLRGLQV--NGSRPGIFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWF 231
   RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGT 291
   21; Gaps
  12 MAHFILFVFTVSTIFHVQQR-----LAKIQAMWELPVQIPVL-----ASTSK 53
   11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
  Redn. of rejection of xenogeneic cells following transplantation by introducing a vector expressing fucosyl:transferase into the cells
H-transferase; xenograft hyperacute rejection; transplantation; glycosyltransferase; galactose alpha(1,3) galactose.
  DB 17; Length 365;
   Squinto SP;
   58.4%; Score 1080.5; DB 17; Lengtl
59.7%; Pred. No. 4.2e-105;
Live 41; Mismatches 79; Indels
   Sandrin MS,
   Rother RP,
   Example 1; Page 45-47; 69pp; English.
  Search completed: May 27, 2003, 15:06:17 Job time: 44.6293 secs
   94US-0278282.
94US-0260201.
  95WO-US07554
   (ALEX-) ALEXION PHARM INC. (AUST-) AUSTIN RES INST.
   Query Match
Best Local Similarity 59.7<sup>3</sup>
Matches 209; Conservative
   Mckenzie IFC,
  WPI; 1996-049326/05
   365 AA;
  N-PSDB; AAT12238
  Homo sapiens
   WO9534202-A1
   21-JUL-1994;
15-JUN-1994;
   14-JUN-1995;
  21-DEC-1995
  Fodor WL,
   Sequence
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RGMWTINAIGRLGNOMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120
  121 RIPWQNYHLNDWMBEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ 180
  MLVVQMPFSFPMAHFILEVFTVSTIFHVQQRLAKIQAKWELPVQIPVLASTSKAJGPSQL 60
  KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF
  VVTSNGMANCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHİIMTIGTFGIWAAYLT
   GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  Query Match
Best Local Similarity 100.
Matches 344; Conservative
  ; ORGANISM: Homo sapiens US-09-298-886-11
   US-09-298-886-11
   LENGTH: 344
  SEQ ID NO 11
  TYPE: PRT
   61
  19
  121
   181
  181
   241
   301
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   ; Search time 14.1436 Seconds
(without alignments)
715.625 Million cell updates/sec
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  US-10-040-863-11
1850
I MLVVQMPFSFPWAHFILFVF......AAFLPEWTGIAADLSPLLKH 344
  Sequence 11,
   Description
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-254-077A-7

US-09-254-077A-7

US-09-298-886-8

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Patent No. 6329170

GENERAL INFORMATION:

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: GAL-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES FILE REFERENCE: 811-029

CURRENT APPLICATION NUMBER: US/09/296,886

CURRENT FILING DATE: 1999-04-26

NUMBER OF SEQ ID NOS: 29

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   APPLICANT: LENNON, GREGORY
APPLICANT: ROUGUIER, SYLVIE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERL-1
TITLE OF INVENTION: GDP-L-FUCOSB: BETA-D-GALACTOSIDE
TITLE OF INVENTION: 2-ALPHA-L-FUCOSYLTRANSFERASES, DNA SEQUENCES ENCODING THE
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   DB 1; Length 343;
  ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
  GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/395,800A FILING DATE: 28-FEB-1995
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Conservative 0; Mismatches 0;
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TELEFEAX: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
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  SEQUENCE CHARACTERISTICS
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CORRESPONDENCE ADDRESS:
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APPLICANT: LOWE,
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US-08-395-800A-8
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   LENGIH:
  Query Match
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   TYPE:
   Best Loca
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RESULT 3 US-09-254-077A-8

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  APPLICANT: SANDRIN, MAURO S.
APPLICANT: SANDRIN, MAURO S.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
CURRENT SPELICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR PPLICATION NUMBER: PCI/AU97/00540
PRIOR FILING DATE: 1999-08-22
PRIOR PLING DATE: 1996-08-23
RIOR FILING DATE: 1996-08-23
SUPHRICK FOR SEQ ID NOS: 12.
SOFTWARE: PATENTIN VOR: 2.1
   APPLICANT: SANDRIN, MAURO S.
APPLICANT: MCKRNZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDÛCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.50SMO
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PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
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Best Local Similarity 99.7
Matches 343; Conservative
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   ; ORGANISM: Sus scrofa
US-09-254-077A-6
                      Patent No. 6399758
GENERAL INFORMATION:
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240 SPVFVVTSNGMAWCREMIDASRGDVVFAGMGLESSPAKDFALLTQVNHTVMTIGTFGIWA 299
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APPLICANT: ELIC H. HOLMES et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT APPLICATION NUMBER: US/09/298,886
NUMBER OF SEQ ID NOS: 29
  APPLICANT: SANDRIN, MAURO S.
APPLICANT: SANDRIN, MAURO S.
APPLICANT: WACKBRIED, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE SPITOPES
FILE REFERENCE: 30562.50SWO
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT APPLICATION NUMBER: PCI/AU97/00540
PRIOR APPLICATION NUMBER: PCI/AU97/00540
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PRIOR FILING DATE: 1996-08-23
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   US-09-298-886-8
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APPLICANT: SANDRIN, MAURO S.
APPLICANT: SANDRIN, MAURO S.
APPLICANT: MCENZIE, IAN C.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.5USWO
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: PCT/AU97/00540
PRIOR FILING DATE: 1997-08-22
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82.0%; Pred. No. 5e-167;
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82.0%; Pred. No. 5e-167;
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Patent No. 5324663
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SOFTWARE: Patentin Ver. 2.1
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LENGTH: 373
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   GENERAL INFORMATION:
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAI GANGLIOSIDE
TITLE OF INVENTION: GAI-SPECIFIC ALPHAI-2 FUCOSYLITRANSFERASE AND USES
FILE REFERENCE: 8511-029
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CURRENT FILING DATE: 1999-04-26
NUMBER OF SEQ ID NGS: 29
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GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
                                SHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSP 316
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   Sequence 12, Application US/09254077A
Patent No. 6399758
Patent No. 6399758
APPLICANT: SANDRIN, MAURO S.
APPLICANT: SANDRIN, MAURO S.
APPLICANT: MCKENZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHXDRATE EPITOPES
FILE REPERBYCE: 30562.5508
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: PCT/AU97/00540
PRIOR PILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: PO 1823
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NUMBER OF SEQUENCES:
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US-08-273-411-1
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  232
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  ă
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  ò
  Db
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  18-08-393-246-6
Sequence 6. Application US/08393246
Sequence 6. Sp55900
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OP INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
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   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington
   ; Score 1080.5; DB 1; Length; Pred. No. 1.5e-115;
41; Mismatches 79; Indels
  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/914,281
  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
NECISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
  PC-DOS/MS-DOS
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSIEM: PC-DOS/MS-
   TELECOMMUNICATION INFORMATION: TELEPHONE: (703)521-4500
   58.4%;
  LENGTH: 365 amino acids TYPE: AMINO ACID
  TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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   Query Match
Best Local $
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OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
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   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
   REGISTRATION NÜMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/220,433
   FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
  US 08/220,433
  NAME: Lavalleye, Jean-Paul M. P.
   TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
   58.4%;
  Floppy disk
  365 amino acids
   12 MAHFILFVFTVSTIFHVQQR-
   TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
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METHODS AND PRODUCTS FOR THE SYNTHESIS OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GENETIDS, OR AS FREE MOLECULES, AND FOR IHE ISOLATION OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
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  DB 1; Length 365;
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  SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/525,058A
FILING DATE:
CLASSIFICATION: 435
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   REFERENCE/POCKET NUMBER: 31,451
TELECOMMUNICATION INFORMATION:
PELEPIONE: (703)521-4EAA
  ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
  PC-DOS/MS-DOS
  Sequence 6, Application US/08525058A Patent No. 5770420
   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
   ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
   (703)521-4500
(703)486-2347
   365 amino acids
  JOHN B.
  APPLICANT: LOWE, JOHN B TITLE OF INVENTION: OF TITLE OF INVENTION: OF TITLE OF INVENTION: OF NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:
   Conservative
   TELEX: 248855 OPAT UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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  CITY: Arlington STATE: Virginia
  amino acid
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  U.S.A.
   Best Local Similarity
Matches 209; Conser
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  US-08-525-058A-6
  COUNTRY:
  TOPOLOGY:
  US-08-525-058A-6
   TELEFAX:
  LENGTH:
   Query Match
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LOCATION: 1.365
OTHER INFORMATION: /note= "GDP-L-fucose:beta-D-Galactoside-2-aipha-L-fucosyl
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  21; Gaps
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   Score 1080.5; DB 1; Length 365;
Pred. No. 1.5e-115;
1; Mismatches 79; Indels 21;
                                    APPLICANT: Gordon, Jeffrey I.
TITLE OF INVENTION: Animal Model for Gastro-Intestinal
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 10
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   SOUTHWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,411
   CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
   *** REFERENCE/DOCKET NUMBER: 31,284

***REFERENCE/DOCKET NUMBER: W0106

***TELEPHONE: (404) 815-6508

***TELEPHONE: (404) 815-6508

INFORMATION FOR SEQ ID NO: 1:

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***LENGTH: 365 amino acids

***TYPE: amino acids

***STRANDEDNESS: single

***TOPOLADY
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   58.4%;
  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,:
   FRAGMENT TYPE: internal
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  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
  MOLECULE TYPE: protein HYPOTHETICAL: NO
GENERAL INFORMATION:
APPLICANT: Falk, Per
   STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
  TOPOLOGY: linear
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APPLICANT: LOWE, JOHN B
APPLICANT: ELNON, GREGORY
APPLICANT: ELNON, GREGORY
APPLICANT: ELNON, GREGORY
APPLICANT: COUNTIER, SYLVIGUE
APPLICANT: ROUGHIER, SYLVIGUE
APPLICANT: RELLY, ROBERT J
ITILE OF INVENTION: 2-ALPHA-L-FUCOSF: BETA-D-GALACTOSIDE
TITLE OF INVENTION: 2-ALPHA-L-FUCOSFILTRANSFERASES, DNA SEQUENCES ENCODING THE
TITLE OF INVENTION: GENOTYPING A PERSON
NUMBER OF SEQUENCES: 22
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  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/395,800A FILING DATE: 28-FEB-1995
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Pred. No. 1.5e-115;
41; Mismatches 79;
  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
   Sequence 10, Application US/08395800A Patent No. 5807732 GENERAL INFORMATION:
   TELECHANICATION: 435
TELECHANICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEFAX: 248855 OPATUR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 59.7
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  Q
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   TILE OF INVENTION: GDP-L-FUCOSE: BETA-D-GALACTOSIDE
TILLE OF INVENTION: 2-ALPHA-L-FUCOSYLTRANSFERASES, DNA SEQUENCES ENCODING THE
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ARLINGTON
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TELEPHONE: (703) 413-220
TELEFAX: (703) 413-220
TELER: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS:
   APPLICANT: LOWE, JOHN B
APPLICANT: LENNON, GREGORY
APPLICANT: ROUGUIER, SYLVIE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERI J
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GenCore version 5.1.4\_p5\_4578 copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-040-863-11

US-09-051-034A-2

US-09-99-672-8

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|                                                                              |                                                                                                       |                                                         | 7777<br>7447<br>7477<br>747                                             |                                                                                                  |                                                          |
|                                                                              | 44444                                                                                                 |                                                         | 4 4 4 4 4 4<br>                                                         |                                                                                                  | ক ক ক<br>ত জ জ                                           |
| 27.70                                                                        | 81.5<br>81.5<br>81.5                                                                                  | 00000                                                   | 300000<br>000000                                                        | 000000                                                                                           | 80<br>80<br>80                                           |
| 20<br>22<br>23<br>23                                                         | 24<br>25<br>27<br>27                                                                                  | 99000                                                   |                                                                         | 8 6 4 4 4<br>8 0 0 1 1 2                                                                         | 444<br>844<br>85                                         |

## ALIGNMENTS

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RGMWTINAIGRLGNOMGEYATLYALAKMNGRPAFIPAOMHSTLAPIFRITLPVLHSATAS 120
  61 RGMWIINAIGRIGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLFVLHSATAS 120
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  GENERAL INFORMATION:

SERVICE INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

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TITLE OF INVENTION:

TITLE OF INVENTION:

PRIOR FILING DATE:

PRIOR FILING DATE:

PRIOR FILING DATE:

TOTAL OF TITLE OF THE 
   Gaps
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0
   Length 344;
   Indels
   100.0%; Score 1850; DB 10;
100.0%; Pred. No. 9.1e-183;
tive 0; Mismatches 0;
                                       Sequence 11, Application US/0999672 Patent No. US20020127655Al
  SOFTWARE: Patentin Ver. 2.0
   Conservative
  NUMBER OF SEQ ID NOS: 29
   ; ORGANISM: Homo sapiens
US-09-999-672-11
  Local Similarity
   SEQ ID NO 11
LENGTH: 344
TYPE: PRT
  344;
US-09-999-672-11
   Query Match
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Query Match
   SOFTWARE: F
SEQ ID NO 8
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  Sequence II, Application US/10040863
Fatent No. US20020137165A1
GENERAL INFORMATION:
TUTLE OF INVENTION: MOLLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GAL-SPECIFIC ALPHA-2 FUCOSYLFRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REPRENSENCE: 8511-029
CURRENT APPLICATION NUMBER: US/10/040,863
CURRENT PILING DATE: 1099-04-23
NUMBER OF SEQ ID NOS: 29
SOFTHARE: PALENTING DATE: 1099-04-23
NUMBER OF SEQ ID NOS: 20
SOFTHARE: PALENTIN OF 20: 2.0
               VVISNGMAWCRENIDISHGDVVFAGDGIEGSPAKDFALLTQCNHIIMIGFFGIWAAYLT 300
  61 RGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120
  RIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ 180
  181 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF 240
  VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT 300
   Gaps
  1 MLVVOMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL 60
   61 RGMWTINAIGREGNQMGEYATLYALAKKNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS
  ;
0
   Length 344;
  Sequence 2, Application US/09051034A

Patent No. US2001005584A1

GENERAL INFORMATION:
APPLICANT: MCKENZIE, IAN FARQUHAR CAMPBELL
APPLICANT: SANDRIN, MAURO SERGIO
TITLE OF INVENTION: GLYCOSYLTRANSFERASE
FILE REFERENCE: 30562.6US40

CURRENT APPLICATION NUMBER: US/09/051,034A

PRIOR APPLICATION NUMBER: PCT/AU97/00452
  Indels
  301 GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
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   Query Match
100.0%; Score 1850; DB 12;
Best Local Similarity 100.0%; Pred. No. 9.1e-183;
Matches 344; Conservative 0; Mismatches 0;
  ORGANISM: Homo sapiens
   RESULT 2
US-10-040-863-11
  SEQ ID NO 11
LENGTH: 344
  US-10-040-863-11
  RESULT 3
US-09-051-034A-2
   TYPE: PRT
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61 RGWWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 126
  RIPWQNYHLNDWMEBEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQBFTLHDHVKEEAQ 180
  181 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF 240
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  1 MLVVQMPFSFPWAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL 60
   Sequence 8, Application US/0999672

Patent No. US20020127655A1

Patent No. US20020127655A1

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: 1039999672

CURRENT APPLICATION NUMBER: US/09/999,672

CURRENT FILING DATE: 2001-10-31

PRIOR APPLICATION NUMBER: US/09/299,886
   50 STSKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI 109
  1 MLVVQMPFSFPMAHFILEVFTVSTIFHVQQRLAKIQAM--WELPV------QIPVLA 49
   12;
  Length 340;
  Ouery Match 79.7%; Score 1475; DB 10; Length 380; Best Local Similarity 77.7%; Pred. No. 5.9e-144; Matches 275; Conservative 30; Mismatches 37; Indels 12
   301 GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  DB 10;
  1.7e-149;
   82.6%; Score 1528; D
82.0%; Pred. No. 1.7e
tive 24; Mismatches
                         60/024,279
  1996-08-21
JMBER: PO1402
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: 60/02
PRIOR FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: P0140
PRIOR FILING DATE: 1996-08-02
NUMBER OF SEQ ID NOS: 14
  PRIOR FILING DATE: 1999-04-26
   Conservative
   TYPE: PRT .
ORGANISM: Rattus norvegicus
  NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
   ORGANISM: Sus Domesticus
  Similarity
  Best Local Simi
Matches 282;
  US-09-051-034A-2
  LENGTH: 340
TYPE: PRT
   RESULT 4
US-09-999-672-8
  LENGTH: 380
   SEQ ID NO 2
  US-09-999-672-8
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  50 STSKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI 109
  110 TLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEF 169
   229
  239
   SLPVLHSDTARKIPWQNYHLNDWMEERYRHI-PGHFVRFTGYPCSWTFYHLRPEILKEF 179
   APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLICSIDE
TITLE OF INVENTION: GAL-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THERROF SET OF FRARYSSLIFVVISNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTI 289
   240 MFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLIGCNHTIMTI 299
  TLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEF 169
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  240 MFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTOCNHTIMTI
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  12;
  GTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLK 343
  Length 380;
  79.7%; Score 1475; DB 12; Lengum. 77.7%; Pred. No. 5.9e-144; Mismatches 37; Indels
   Sequence 8, Application US/10040863 Patent No. US20020137165A1 GENERAL INFORMATION:
   TYPE: PRT; ORGANISM: Rattus norvegicus
US-10-040-863-8
   Matches 275; Conservative
   Similarity
   LENGTH: 380
  US-10-040-863-8
   Query Match
Best Local &
   170
   300
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RESULT 6 US-09-999-672-10

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; Sequence 10, Application US/0999672; Patent No. US20020127655A1; Patent No. US20020127655A1; GENERAL INFORMATION:
APPLICANT ETIC H. Holmes et al.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE; TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 9511-029
CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT FILING DATE: 1999-01-10-31
PRIOR APPLICATION NUMBER: US/09/296,886
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 20
   GEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLNDWMEEE 136
   137 YRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRGLQVNGSRPGIF 196
  US-10-040-863-10
Sequence 10, Application US/10040863
Fatent No. US20020137165A1
GENERAL INFORMATION:
TITLE OF INVENTION: MUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLFRANSFERASE AND USES;
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/10/040,863
CURRENT APPLICATION NUMBER: 09/298,886
PRIOR APPLICATION NUMBER: 09/298,886
PRIOR FILING DATE: 1999-04-23
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   28 VQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRCMWTINAIGRLGNQM 76
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  DB 10;
  Score 1376; DB 10
Pred. No. 9e~134;
6; Mismatches 31
  317 FLKIFKPEAAFLPEWTGIAADLSPLLK 343
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78.98;
  ; ORGANISM: Rattus norvegicus
US-09-999-672-10
   ORGANISM: Rattus norvegicus
   SOFTWARE: Patentin Ver. 2.0
   Conservative
   NUMBER OF SEQ ID NOS: 29
   Query Match
Best Local Similarity
  Similarity
  US-10-040-863-10
  SEQ ID NO 10
LENGTH: 353
   Matches 258;
  SEQ ID NO 10
LENGTH: 353
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. John
J. Michael
Animal Tissue with Carbohydrate Antigens Compatible for Human
Transplantation and a Carbohydrate Determinant Selection Syst
Recombination
   1.1, PETER
N: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
N: RESISTANT TO FIR E. COLI ASSOCIATED DISEASES
ON NUMBER: US/09/844,705
TE: 2001-04-27
I: 1999-11-19
NOS: 13
IN VOET: 2.0
  3;
   RITLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFIGYPC 153
   58.5%; Score 1081.5; DB 10; Length 365; 65.5%; Pred. No. 2.6e-103; ative 30; Mismatches 66; Indels 11; Gaps
   ----SKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPA 93
   7002
NUMBER: US/10/105,963
: 2002-03-21
NHBER: US 60/277,811
ton US/09844705
336A1
   on US/10105963
  oration
  Chris
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54 ALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV 113
   231
   Gaps
   --- ASTSK 53
  11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
  42 PVQIPVLAST-----SKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPA 93
   114 LHSATASRIPWQNYHLNDWMEEEFRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD
  HVREEAQKFLRGLQV--NGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWF
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  58.1%; Score 1075.5; DB 10; Length 365; 65.2%; Pred. No. 1.1e-102;
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   FGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPL 341
   Indels
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   DB 10;
  58.4%; Score 1080.5; DB 1
59.7%; Pred. No. 3.3e-103;
tive 41; Mismatches 79;
   30; Mismatches
   GENERAL INFORMATION:
APPLICANT: MCKEMZIE, IAN FAROUHAR CAMPBELL
APPLICANT: SANDRIN, MAURO SERGIO
TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS
TITLE OF INVENTION: GLYCOSYLTRANSFERASE
   FILE REFERENCE: 30562.60SWO
CURRENT APPLICATION NUMBER: US/09/051,034A
CURRENT FILING DATE: 1998-03-31
   MBER: PCT/AU97/00492
1997-08-01
MBER: 60/024,279
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  SEQUENCE DESCRIPTION: SEQ ID NO: US-09-863-475A-6
   PRIOR APPLICATION NUMBER: PCT/AU97, PRIOR FILING DATE: 1997-08-01 PRIOR APPLICATION NUMBER: 60/024,27 PRIOR FILING DATE: 1996-08-21 PRIOR APPLICATION NUMBER: PO1402 PRIOR FILING DATE: 1996-08-02 NUMBER OF SEQ ID NOS: 14
   Sequence 4, Application US/09051034A Patent No. US20010055584A1
TELEPHONE: (703)521-4500
              TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acid
TYPE: amino acid
  TOPOLOGY: unknown MOLECULE TYPE: protein
  Best Local Similarity 65.2% Matches 202; Conservative
  Local Similarity 59.77
   Sus Domesticus
  Patentin Ver.
   US-09-051-034A-4
  US-09-051-034A-4
  365
  SOFTWARE:
SEQ ID NO 4
   ORGANISM:
  TYPE: PRT
   Query Match
   Query Match
  LENGTH:
   Matches
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   232
   250
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   Sequence 6, Application US/09863475A

Patent No. US20020105688A1

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS

OF OLIGOASCCHARIDE STRUCTURES ON GLYCOPROTEINS,

GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION

OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
  4;
  249
   189
  291
   54 ALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV 113
  114 LHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD 173
   231
  Gaps
  -- ASTSK 53
   11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPFVAIFCLPGTAMGPNASSSC 70
   RARYSSL1FVVTSNGMAWCRENIDTSHGDVVFAGDG1EGSPAKDFALLTQCNHT1MT1GT
   174 HVREEAQKFILKGLQV--NGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWF
   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
  21;
   Length 365;
  292 FGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPL 341
  P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
  Indels
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  -LAKIQAMWELPVQIPVL
   DB 9;
   58.4%; Score 1080.5; DB 9; 59.7%; Pred. No. 3.3e-103; iive 41; Mismatches 79;
   NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
  APPLICATION NUMBER: US/09/863,475P
   APPLICATION NUMBER: 07/914,281
   FILING DATE: 24-May-2001 CLASSIFICATION: <Unknown>
   TELECOMMUNICATION INFORMATION:
  FILING DATE: 20-JUL-1992 ATTORNEY/AGENT INFORMATION:
                     SOFTWARE: Patentin version 3.1
   COMPUTER READABLE FORM:
  PRIOR APPLICATION DATA:
   NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS
   12 MAHFILFVFTVSTIFHVQQR-
   Best_Local Similarity 59.7
Matches 209; Conservative
  CITY: Arlington
   STATE: Virginia
  COUNTRY: U.S.A.
NUMBER OF SEQ ID NOS: 40
  TYPE: PRT
ORGANISM: Homo sapiens
US-10-105-963-10
   ZIP: 22202
  US-09-863-475A-6
  SEQ ID NO 10
LENGTH: 365
   Query Match
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RESULT 14

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15;
   15;
Sequence 14, Application US/09479614
Publication No. US20030013183A1
GENERAL INFORMATION
APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT APPLICATION NUMBER: 60/115,033
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER FILING DATE: 1999-01-07
NUMBER OF SECIL DOS: 34
   APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-10.47
CURRENT APPLICATION NUMBER: US/09/479,614
EARLIER PAPPLICATION NUMBER: 60/115,033
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
  102 VSACTMNFIPPIVKLFHSSCNPLGDTG-----STIQLLCLISG---YVPGDMEVTWLVD 152
  103 ---LAPIFRITLPVLHSATASRIPWQNYHLNDWMEBEYRHIPPGEYVRFTGYPCSWTFYH 159
   160 HIRQEILQEFTLHDHVREEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVA 219
   278 LLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSP-----FLKI----FKPEA-A 326
  153 GOKAINIFPYTAP---GKQEGKVISTHSELN------ITQGEWVSQKTYTCQVTY-- 198
  220 DRRYLQQALDWFRARYSSLIFVVTSNGM--AWCRENIDTSHGDVVFAGDGIEGSPAKDFA 277
   93; Gaps
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   6.5%; Score 119.5; DB 9; Usength 496; 23.8%; Pred. No. 0.001; Live 27; Mismatches 111; Indels 93
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   Query Match 6.5%; Score 119.5; DB 9; Best Local Similarity 23.8%; Pred. No. 0.00084; Matches 72; Conservative 27; Mismatches 111;
   ------LANTDGMILTWSRENGESVHPD-
  Sequence 2, Application US/09479614 Publication No. US20030013183A1
  SOFTWARE: Patentin Ver. 2.0
   Query Match 6.5
Best Local Similarity 23.8
Matches 72; Conservative
  TYPE: PRT
ORGANISM: Felis catus
   ; TYPE: PRT; ORGANISM: Felis catus
US-09-479-614-14
  GENERAL INFORMATION:
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   329 FLP 331
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Search completed: May 27, 2003, 15:25:45 Job time : 16.8627 secs

327 FLP 329 ||| 394 FLP 396

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   May 27, 2003, 15:00:45; Search time 12.4655 Seconds (without alignments) 2652.940 Million cell updates/sec
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   Description
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
  Total number of hits satisfying chosen parameters:
  283224 segs, 96134422 residues
   SUMMARIES
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
   A56098
B56392
A56392
A36047
S46494
S51582
T447328
H87911
   T25390
T22068
T25307
T25309
   T31916
T32294
H71976
T25334
   T02798
T21051
  BLOSUM62
Gapop 10.0 , Gapext 0.5
   ΩĮ
  seq length: 0
seq length: 2000000000
   US-10-040-863-11
1850
  DB
  Query
Match Length
   PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
   1832.5
10803.5
10803.5
1080.15
623
623
181.5
144.5
144.5
137.5
137.5
120.5
120.5
120.5
110.0
1115.5
1115.5
1115.5
1116.1
  Title:
Perfect score:
Sequence:
  Score
   Scoring table:
   Minimum DB :
Maximum DB :
  Database :
  Searched:
  Result
  Run on:
```

| hypothetical prote | hypothetical prote | glycoprotein 6-alp | pol polyprotein - | hypothetical prote | beta-glucosidase ( | DNA helicase YGL15 | L-carnitine dehydr | DNA polymerase III | allantoinase (EC 3 | virB4 protein prec | conserved hypothet | hypothetical prote | hypothetical prote | probable copper-tr | metalloproteinase, |  |
|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--|
| T34406             | H84828             | JC5432             | S32437            | E72398             | JC5137             | S60416             | D69252             | AH3171             | A53595             | E97717             | AC2861             | B97638             | A84556             | G70978             | A72012             |  |
| 7                  | 7                  | г                  | H                 | ~                  | N                  | 7                  | ~                  | N                  | Н                  | 7                  | ~                  | 7                  | 7                  | 7                  | 7                  |  |
| 339                | 401                | 575                | 1462              | 451                | 460                | 1489               | 420                | 1085               | 483                | 802                | 252                | 276                | 396                | 718                | 974                |  |
| 4.9                | 4.9                | 4.0                | 4.8               | 4.8                | 4.8                | 4.8                | 4.7                | 4.7                | 4.7                | 4.7                | 4.6                | 4.6                | 4.6                | 4.6                | 4.6                |  |
| 91                 | 91                 | 06                 | 89.5              | 8                  | 83                 | 8                  | 87.5               | 8.7                | 86.5               | 86.5               | 85.5               | 85.5               | 85                 | 85                 | 85                 |  |
| 3.0                | 31                 | 32                 | m                 | 3.4                | 3.5                | 98                 | 3.7                | ac<br>r            | о Ф<br>( M         | 40                 | 4                  | 42                 | 43                 | 44                 | 45                 |  |
|                    |                    |                    |                   |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |  |

## ALIGNMENTS

|                                                                                                                                                                                                                                                                      | group al               |                                                                                                                                                             |                                                                                                                                                                                     | 1;                                                                                                                                                            |                                                                          |                                                                            |                                                                                                                                              |                                                                         |                                                                                                            |                                                            |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------|----------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|------------------------------------------------------------|
| RESULT 1 A56098 alpha(1,2)fucosyltransferase Sec2, long form - human C;Species: Homo sapiens (man) C;Date: 03-0ct-1995 #sequence_revision 03-0ct-1995 #text_change 21-Jul-2000 C;Date: 03-0ct-1998 R;Kelly, R.J.; Rouquier, S.; Giorgi, D.; Lennon, G.G.; Lowe, J.B. | e human Secretor blood | A;Status: preliminary<br>A;Molecule type: DNA<br>A;Residues: 1-343 <kel><br/>A;Cross-references: GB:U17894; NID:g687618; PIDN:AAC24453.1; PID:g687619</kel> | Cydenetics: A,Genetics: A)Genetics: SE A,Cross-references: GDB.120619, OMIM:182100 A,Map position: 19q13.3-19q13.3 C;Keywords: glycoprotein; Golgi apparatus; transmembrane protein | Query Match 99.1%; Score 1832.5; DB 2; Length 343; Best Local Similarity 99.7%; Pred. No. 5.7e-149; Matches 343; Conservative 0; Mismatches 0; Indels 1; Gaps | QY 1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVIASTSKALGPSOL 60<br> | QY 61 RGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120<br> | QY 121 RIPWQNYHLNDWMEEEYRHIPPGEXVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ 180 121 RIPWQNYHLNDWMEEEYRHI-PGEXVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ 179 | QY 181 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF 240 | QY 241 VVTSNGMAWCRENIDTSHGDVVFAGDGIBGSPAKDFALLTQCNHTİMTIGTFGIRAAYLT 300 1111111111111111111111111111111111 | Qy 301 GGDTIYLANYTLPDSPPLKIFKPEAAFLPEWTGIAADLSPLKH 344<br> |

RESULT

| 0y         161 LROEILQEFTLHDHVREEAQKFLRGLQVNGSRPGTFVGYHVRGDYVHVMPKVWKGVV         218           177 VREQIRREFTLHDHLREEAQRLLGKLGKLGRTGARPRTFVGYHVRRGDYLQVMPQRWKGVV         236           0y         219 ADRRYLQQALDWFRARXSSLIFVYTSNGMAWCRENIDTSHGDVYFAGDGIEGSPAKDFAL         278           1  1  1  1  1  1  1  1  1  1  1  1  1  1 | Best Local Similarity 5 Secret 1080.5 DB 2; Length 365; Resylorasine Procession Procession Sequence—revision 16-Nov-1990 #text_change 10-Sep-19. Accession: A66047 | QY 114 LHSATASRIPWQNYHLNDWMBEEYRHIPPGEYVRFTGYPGSWTFYHHLRQEILQEFTLHD 173                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| galactoside<br>cies: Orycto<br>es: 19-Oct-11<br>es: 10-Oct-11<br>oshi, S.; K<br>Ol. Chem. 2;<br>Ol. Chem. 2;<br>Ol. Chem. 2;<br>It Molecula<br>erence numble<br>ession: B56<br>etus: prelim:<br>ctus: prelim:<br>ctus: prelim:<br>ctus: prelim:<br>ctus: reference<br>words: trans                                                | 110; 41; 41; ISKALGP ITTLPVLH  :                                                                                                                                   | Deta-galactoside alphai, 2-fuccsyltransferase I - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Species: Oryctolagus cuniculus (domestic rabbit) C;Species: 19-0ct-1995 #sequence_revision 19-0ct-1995 #text_change 05-Nov-1999 C;Accession: A56392 A;Hitoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S. T;Hitoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S. A;Title: Molecular cloning and expression of two types of rabbit beta-galactoside alphai A;Reference number: A56392; MUID:95238380; PMID:7721792 A;Status: preliminary A;Molecula type: mRNA A;Residues: 1-373 <hit> A;Residues: 1-373 <hit> A;Residues: 1-373 <hit> A;Cross-references: GB:X80226; NID:9854354; PIDN:CAA56513.1; PID:9854355 C;Keywords: transmembrane protein Query Match Best Local Similarity 67.0%; Pred. No. 9.6e-86; Matches 203; Conservative 38; Mismatches 59; Indels 3; Gaps 2; A1 LPVQIPVLASTSKALGPSQLRGMWTINAIGRIGNQMGEYATLYALAKMNGRPAFIPAQHH 100                                      </hit></hit></hit> |

14;

Gaps

62;

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R;Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Gene 237, 321-332, 1999
A;Title: The genes responsible for O-antigen synthesis of Vibrio cholerae Ol39 are classecree number: 222749; MUID:99453293; PMID:10521656
A;Reference number: 222749; MUID:99453293; PMID:10521656
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-281 < YAM>
  A,Cross-references: EMBL:AB012957; NID:q4115688; PIDN:BAA33632.1; PID:g3721682
A;Experimental source: strain 022
C;Genetics:
   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-363 <WILD.
A;Coss-references: EMBL:292830; PIDN:CAB07352.1; GSPDB:GN00023; CESP:F11A5.5
A;Experimental source: clone F11A5
   C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T20745
     21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 28-Jul-2000
  68 KGSSNRLSRILRRLGW--LKKNTYYAEKÕRTIYDVSVFMQAPRYL--DGYWQNEQYFSQI 123
   70 --GRLGNQMGEYATLYALAKMNGR-PAFIPAQMH-----STÜÄPIFRITLPVLHSAT 118
  -----SATASRIPWQNYHLNDWMEEEYRHI------PPGEYVRFTGYPCSWTFYHHL 161
   222 RYLQQALDWFRARYSSLIFVVTSNGMAWCREN---IDTSHGDVVFAGDGIEGSPAKDFAL 278
   175 DYYKRAVDYIKEKIEAPVFFVFSNDVAWCKDNFNFIDSP----VFIED--TQTEIDDLML 228
  78 SSSRLGNHLFELASVLSISRELQRVPTFFIENCYHEKMWEDSNTLIPGLMNHFLIINGSV 137
  16 ILFVFTVSTIFHVQQRLAKIQAMWEL-PVQIPVLASTSKALGPSQLRGMWTINAI---- 69
   33 LFWMILVYSIF-----LIRAMHEEDPMEVP------YPPAQINFRISRKYISSNYA 77
   8 GGLGNOLFQYAVGRAIAIQYGVPLKLDVSAYKNYKLHNGYRLDQFNINADIANEDEIFHL 67
   162 RQEILQEFILHDHVREEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADR
  Indels 117;
  A;Map position: 5
A;Introns: 42/1; 55/2; 136/3; 175/3; 210/2; 243/1; 299/1; 330/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
   70 GRIGNOMGEYATLYALAKMNGRP-----AFIPAQMHSTL-APIFRITLPVLH---
   9.8%; Score 181.5; DB 2; Length 363; 23.3%; Pred. No. 8.6e-08;
   Length 281;
  229 MCQCQHNIVANSSFSWWAAWLNSNVDKIVIAPKTWMAENPKGYKWVPDS 277
  Ouery Match 10.5%; Score 195; DB 2; Length 28 Best Local Similarity 26.6%; Pred. No. 4.4e-09; Matches 77; Conservative 46; Mismatches 104; Indels
   A;Note: wblA
C;Superfamily: Vibrio cholerae hypothetical protein wblA
   54; Mismatches 116;
   hypothetical protein F11A5.5 - Caenorhabditis elegans
   279 LTQCNHTIMTIGTFGIWAAYLTGG-DTIYLANYT----
  submitted to the EMBL Data Library, March 1997
A;Reference number: 219319
A;Accession: T20745
  Conservative
   Similarity
  A; Gene: CESP:F11A5.5
              C;Date: 21-Jan-2000
C;Accession: T44328
  87;
  Query Match
Best Local
   C; Genetics:
  116
  Matches
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   R.Piau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
Blochem. J. 300, 623-626, 1994
A;Title: Evidence for two distinct alpha-(1,2)-fucosyltransferase genes differentially
A;Reference number: $46493; MUID:94280382; PMID:8010942
A;Status: preliminary
A;Title: Evidence for two distinct alpha-(1,2)-fucosyltransferase genes differentially A;Reference number: S46493; MJID:94280382; PMID:8010942
A;Accession: S46494
   ..
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  ö
   galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 17-Nov-1995 #text_change 08-Oct-1999
   A;Molecule type: mRNA
A;Residues: 1-142 <PIA>
A;Cross-references: EMBL:L26009; NID:g414814; PIDN:AAB41514.1; PID:g554438
   PCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRGLQVN--GSRPGTFVGVHVRRGDYVHV 209
  210 MPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIE 269
   Gaps
   A.Cross-references: EMBL:L26010; NID:g414816; PIDN:AAB41515.1; PID:g414817 C;Genetics:
  213 VWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAMCRENIDTSHGDVVFAGDGIEGSP 272
  273 AKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWT 332
  62 AKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIXLANYTLPDSPFLKVFKPEAAFLPEWV 121
  Gaps
   2 VWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDGVFAGNGIEGSP 61
  ..
  Length 142;
  Length 159;
  Query Match 32.1%; Score 593; DB 2; Length 14 Best Local Similarity 74.6%; Pred. No. 1.7e-43; Matches 106; Conservative 16; Mismatches 18; Indels
  Indels
  T44328
hypothetical protein wblA [imported] - Vibrio cholerae
C;Species: Vibrio cholerae
   C;Accession: 551502; S46493
C;Accession: 551502; S46493
R;Piau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
submitted to the EMBL Data Library, November 1993
A;Reference number: S51582
A;Accession: 551582
   Score 623; DB 2; L. Pred. No. 5.3e-46; 6; Mismatches 9;
   A, Cross-references: EMBL:L26009
C; Keywords: glycosyltransferase; hexosyltransferase
  A;Gene: FTB
C;Keywords: glycosyltransferase; hexosyltransferase
  270 GSPAKDFALLTQCNHTIMTIGT 291
  Query Match 33.7%;
Best Local Similarity 88.5%;
Matches 116; Conservative
  122 GIPADLSPLLK 132
   333 GIAADLSPLLK 343
   A; Molecule type: mRNA
A; Residues: 9-135 <P12>
  A; Molecule type: mRNA
A; Residues: 1-159 <PIA>
   A;Status: preliminary
  61
   121
  RESULT 7
   RESULT 6
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| Db 369 LHFFCPGPREVDMAILKSCDSVIISTGTFGWWGAYLNVNASPDVYYKHWPAPGSVM 425 QY 318 LKIEKPEAAFLPEWTG1 334 | Status: Status: Molecul Molecul Cross-rr Experim Genetic Gene: CI Map pos: Introns Superfan Ouery M Matches 80 75     | Oy 133 MEBEYRHIPPGEYVRFIGYPCSWTFYHHLROEILQEFTLHDHVREEAQKFLRGLQVNGSR 192  Db 170                                                                                     |
|--------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| LLRG<br>LLRG<br>CNH<br>CNH<br>CDV                                                                | SULT<br>7911<br>7911<br>57911<br>57911<br>5791<br>5791<br>6701<br>6701<br>6701<br>6701<br>6701<br>6701<br>6701<br>670 | Query Match Best Local Similarity 20.4%; Pred. No. 3.38-07; Matches 89; Conservative 63; Mismatches 145; Indels 140; Gaps 17;  Qy 15 FILFVFTVSTIFHVQDRLAKI-QANWELPV |

| DD 121 INTRCCVEVDPLIN QY 177 EEAQKFLRGLQVNG                                                        | 2.4 Db 164GYLKTSENFG Qy 232 RARYSSLIFVVTSN Db 207 IRKAKEFV                                                                                                                                                                 |                                                                                                     | Db 253 SPSDDLVYAKNNCD Oy 321FKPEAAFLE                                                                                                                        | Db 303 YENGGLNPYDYYLE                                        | #55051 15 #171976 probable alpha(1,2)fucos (Species: #elicobacter ) vianietus etrain 199 | C.Date: 12-Feb-1999 #sec<br>C.Paccession: H71976<br>E.Alm, R.A.; Ling, L.S.1<br>F.Alm, R.A.; Ling, L.S.1 | Nature 397, 176-180, 198<br>A,Title: Genomic sequent<br>A,Reference number: A71                                                         | A; Accession: 1.1270 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-299 <arn> A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cross references: GB: A; Cr</arn> | C;Genetics: A;Genetics: A;Gene: jhp0086 C;Superfamily: Vibrio cl             | Query Match Best Local Similarity Matches 67; Conser                                                                                                                                                                                    | 9 XO                                                                                                                                                                                          | Db 6 VQICGGLGNQMFQ Ov 121 RIP-WONYHLNDW       | 22<br>Db 63                                                                                                                                | OY 162 ROEILOEFIL 0y 162 ROEILOEFIL 0                                                                           | ζŏ                                                                                                                                                                                                      | Db 175 GCQLGIDYQKRAV                             | 20; QY 276 FALLTQCNHTIMT                                                                                        | Db 234 MLLMGSCKHGIIA                                               | QY 334 I 334                                            | Db 286 I 286                                                                         | RESULT 14<br>T25334<br>hypothetical protein T2       |
|----------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------|-----------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------|---------------------------------------------------------|--------------------------------------------------------------------------------------|------------------------------------------------------|
| A;Accession: T31916<br>A;Status: preliminary; translated from GB/EMBL/DDBJ<br>A;Molecule type: DNA | A; Residues: 1-348 <sam> A; Cross-references: EMBL:AF016654; PIDN:AAB66030.1; GSPDB:GN00020; CESP:C17A2 A; Experimental source: strain Bristol N2; clone C17A2 C; Genetics: A; Gene: CESP:C17A2.4 A; Map position: 2</sam> | ntrons: 94/3; 133/3: 168/2: 272/1<br>perfamily: Caenorhabditis elegans hypothetical protein C14C6.3 | Query Match 7.8%; Score 144.5; DB 2; Length 348; Best Local Similarity 22.1%; Pred. No. 0.00012; Matches 62; Conservative 61; Mismatches 86; Indels 71; Gaps | 71 RLGNQMGEYATLXALA-KMNGRPAF-IPAQMHSTLAPIFRITLPVLHSATASR 121 | 122 IPWQNYHLNDWMEEEYRHIPPGEYVRFTG-YPCSWTFYHHLRQEILQEFT 170                               | 171 LHDHVREBAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGV-VADRRYL 224   : :                                    | 225 QQALDWFRARXSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIE 269 :::       :     :   :     :     :     :     :     :         :       :           : | 270 GSPAKDFALLTQ-CNHTIMTIGTFGIWAAYLFGGDTIY 306<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | RESULT 12<br>T32294<br>hypothetical protein K06H6.6 - Caenorhabditis elegans | pecies: Caenorhabdilis elegans<br>ate: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 20-Jun-2000<br>cession: T32294 #sequence_revision 29-0ct-1999 #text_change 20-Jun-2000<br>parid M · Wohldmann, P : Bauer. C.: Clarke, K. | A, Daylu, M., Mollamann, F., Dayle, C., Carlotte, C., Asherited to the EMBL Data Library, September 1997 A, Description: The sequence of C. elegans cosmid K06H6. A: Reference number: 221147 | coession: T32294 translated from GB/EMBL/DDBJ | tesiduss: 1-335 <dav<br>tesiduss: 1-335 <dav<br>toss-references: EMBL:AF024500; PIDN:AAB70365.1; GSPDB:GN00023; CESP:K06</dav<br></dav<br> | <pre>Xxperimental source: strain bristol N2; clone Kuoho enetics: Anetics: Anetics: Anetics: CESP:R06H6.6</pre> | <pre>dap POSILION: 3 Introns: 17/1; 32/2; 58/1; 111/3; 150/3; 184/2; 218/1; 243/3; 272/1; 303/ introns: 17/1; 32/2; 58/1; 111/3; liperfamily: Caenorhabditis elegans hypothetical protein C14C6.3</pre> | Query Match 7.6%; Score 141.5; DB 2; Length 335; | Best Local Similarity 20.4%; Fred. No. 0.0002;<br>Matches 77; Conservative 53; Mismatches 118; Indels 129; Gaps | 16 ILFVETVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQLRGMWTINAIGRLGNQ 75 | 12 VLLVLTLVIVVQLYKSATAEIPPLRQESFLIMKKRLSSRMAPTARLGNH 60 | 76 MGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYH 128       : ::      :  :  : | 129 LNDMMEESYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVR |
| A S A                                                                                              | A P C P P P P P P P P P P P P P P P P P                                                                                                                                                                                    | A;I                                                                                                 | CMZ                                                                                                                                                          | Qy                                                           | S<br>S                                                                                   | QY                                                                                                       | QY                                                                                                                                      | Qy<br>Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | RES<br>T32<br>hyp                                                            | 0000                                                                                                                                                                                                                                    | sul<br>A;I                                                                                                                                                                                    | A A                                           | AAA                                                                                                                                        | AUA,                                                                                                            | ά <b>ἀ</b> δ                                                                                                                                                                                            |                                                  |                                                                                                                 | Qy                                                                 | qq                                                      | 0 <i>y</i>                                                                           | QY                                                   |

| Ор             | 121 LNTRCCVFVDPLIHEHNNDEYLHL-DGREYQAWKYFPSMRNELI 163                                                                                                                                                   |
|----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Qy             | MPKVWKGVVADRRYLQQAL                                                                                                                                                                                    |
| OD             | 164GYLKISENFGSLPKSNEISFVICVHIRRGDFKRVGFAESDEWF 206                                                                                                                                                     |
| Qy<br>dq       | 232 RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIE                                                                                                                                                             |
| ã ŏ î          | 71 SPAKDFALL-TQCNHTIMIGTEGIWAAYLT                                                                                                                                                                      |
| a c            |                                                                                                                                                                                                        |
| op<br>C        | 03 YRNGGLNPYDYYLPHWT 31                                                                                                                                                                                |
| RESULT         | LT 13                                                                                                                                                                                                  |
| Prok<br>C; Sp  | H.1976<br>probable alpha(1,2)fucosyltransferase - Helicobacter pylori (strain J95)<br>C.Species: Helicobacter pylori                                                                                   |
| A; Va<br>C; Da | nriety: strain J99<br>ste: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000                                                                                                         |
| C; AC<br>R; AJ | C;Accession: H71976<br>RyAlm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.<br>• Tose, C. : Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F |
| Natu<br>A,Tj   | 999<br>nce comparison of two unrelated isolates<br>1800; MUID:99120557; PMID:9923682                                                                                                                   |
| A; Ac          | H71976                                                                                                                                                                                                 |
| A; R¢          | e: DNA<br>299 <arn><br/>nces: GB:AE001447;</arn>                                                                                                                                                       |
| A C A          | cal source: strain JS9<br>กกล                                                                                                                                                                          |
| A; S:          | LY:                                                                                                                                                                                                    |
| ŌĂĬ            | Query Match 7.5%; Score 138; DB 2; Length 299; Best Local Similarity 22.3%; Pred. No. 0.00035; Matches 67; Conservative 45; Mismatches 137; Indels 52; Gaps 11;                                        |
| Qy             | 66 INAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120                                                                                                                                         |
| qq             | FOYAFAKSLOKHSNIPVLLDIISFDGSNRKMQLELFPIDLPYA                                                                                                                                                            |
| δy             | ٠٠ ت                                                                                                                                                                                                   |
| QQ             | 12                                                                                                                                                                                                     |
| OY             | RQEILQEFILHDHVREEAQKFLRGLQ-VNGSRPGTFVGVHVRRGDYVHVMPKVWK 21                                                                                                                                             |
| qq             | 123 SSLIKOTFTLPPPPENGNNKKKEEEFHRKLSLILAAKNSVFAHIRRGDYVGI 174                                                                                                                                           |
| QY             |                                                                                                                                                                                                        |
| qq             | 175 GCQLGIDYQKKAVEYMAKRVPNMELFVFCEDLKF-TQNLDLGYPFMDMTTRDKDEBAYWD 233                                                                                                                                   |
| δŽ             | $\sim$                                                                                                                                                                                                 |
| QQ             | 234 MILMOSCKHGIIANSTYSWWAAYLINNPGKIIIGPKHWLFGHENILCKEWVK 285                                                                                                                                           |
| ΟŸ             | 334 1 334                                                                                                                                                                                              |
| qq             | 286 I 286                                                                                                                                                                                              |
| RES            | CULT 14                                                                                                                                                                                                |
| T25<br>hyp     | 125334<br>hypothetical protein T26H5.8 - Caenorhabditis elegans                                                                                                                                        |
|                |                                                                                                                                                                                                        |

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   C;Species: Lefshmania major (C;Species: Lefshmania major (C;Species: Lefshmania major (C;Species: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000 (C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000 (C;Date: 24-May-2000   A; Residues: 1-348 <PYL>
A; Cross-references: GB:AE001274; NID: 93264850; PIDN:AAC24622.1; PID: 92978459; GSPDB:GNOG C; Genetics:
  18;
  A:Cross-references: EMBL:282056; PIDN:CAB04857.1; GSPDB:GN00023; CESP:T26H5.8 R;Wall, M.
C:Species: Caenorhabditis elegans
C:Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C:Accession: T25334; I26£00
   A; Introns: 771; 32/3; 55/1; 109/3; 148/3; 187/2; 222/1; 263/1; 333/1; 363/3
C; Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
   hypothetical protein L549.10 [imported] - Leishmania major (strain Friedlin)
   72 LGNQMGEYATLYALAKMNGRPAFIPA-----QMHSTLAPIF-----RITLPVLHSATA 119
  120 SR--IPWQNYHLND----WMEEEYRH-IPPGBYVRFTGYPCSWTFYHHLRQEILQEFTLH 172
  173 DHVREEAQKFLRGLQVNGSRPGTFVGVHVRRGDY----VHVMPKVWKGVVADRRYLQQAL 228
   ----TQCNHTIMT--I 289
   54 LGNRLFELISLIGIASTLQRRAVINATNPNYMSHLHQTMQPLFPKLVEQFELRVIPESSV
  229 DWFRARYSS----LIFVVTSNGMA--------WCRENIDISH--GDVVFAGDG-
  Score 137.5; DB 2; Length 392;
Pred. No. 0.00055;
   A; Residues: 1-392 <WI2>
A;Cross-references: EMBL:AL032620; PIDN:CAA21488.1; CESP:T26H5.8
A;Experimental source: clone Y36E3A
  Indels
  |||| | :|| :|| :| STFGWWLSYLAKSSAKVYYRDILETKDGVINDMKVEDFYPPEW 378
  290 GTFGIWAAYLTGGDT-IYLANYTLPDSPFLKIFKPEAAFLPEW 331
   7.4%, Score ... 0.0000...
21.0%; Pred. No. 0.0000...
***a 56; Mismatches 114;
  A Status: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: DNA A, Residues: 1-392 < WILD-A;Cross-references: EMBL:282056; PIDN:CAB04857 1 . G
   A/Reference number: 220243
A/Accession: T26600
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
  Submitted to the EMBL Data Library, November 1996
A;Reference number: 220017
A;Accession: T25334
   submitted to the EMBL Data Library, October 1998
   268 -----KDFALL---
   Query Match
Best Local Similarity 21.09
Matches 72; Conservative
  A; Status: preliminary A; Molecule type: DNA
  A; Gene: CESP: T26H5.8
  A; Map position: 5
  336
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73 TLFRDLGHYGVQMCASSPPLPVVTVPBTRPVRKVQLDAQRPCVFHMIGFFQSDAFFDDHP 132
   ATASRIP---WQN-----YHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEIL 166
  133 IMSSVIPRELWDSAGKHLATYYGGGSCHTVALHVRRGDYTRFT-------DIF 178
   Gaps
  207 VHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFV----VTSNGMAWCRENIDISHGDVV 262
   263 FAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFK 322
  ---GSRPGTFVGVHVRRGDY 206
  284 MPRDVLE-----LLMMSQCNDVVMANSTFSWWGAYL---NRVSLRRVIAPSRNFVKDPY 334
   Indels '131;
  Length 348;
   54 ALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPA
  7.1%; Score 131.5; DB 2;
18.1%; Pred. No. 0.0015;
Live 48; Mismatches 125;
   ---QMHSTLAPIFRITLPVL-----
   Search completed: May 27, 2003, 15:08:20 Job time : 14.4655 secs
  QEFTLHDHVREEAQKFLRGLQVN---
   Conservative
  323 PEA--AFLPEW 331
   335 PASNHLYCPGW 345
   Query Match
Best Local Similarity
Matches 67; Conserv
A:Gene: L549.10
A;Map position: 1
```

```
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

May 27, 2003, 14:53:11; Search time 10.0683 Seconds (without alignments) 1417.108 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-040-863-11 1850 1 MLYVQMPFSFPMAHFILFVF......AAFLPEWTGIAADLSPLLKH 344

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched: 112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|           | ption                | Q10981 h galactosi | sns      | Q28113 bos taurus | oryc       | Ш          | Q10980 rattus norv | oryc       | mus π  | рошс       |          |          | P34302 caenorhabdi | P79282 s alpha-(1, | Q9byc5 h alpha-(1, | Q9wts2 m alpha-(1, | saccharomy | P40757 rana catesb | ralstonia  | P96875 mycobacteri | O35899 cavia porce | 002350 anopheles g |            | Q9jqx3 neisseria m | Φ    |            | S          |         | ч          | arabidc    | E          | rattus no | nomo sapi      | salmonel   |
|-----------|----------------------|--------------------|----------|-------------------|------------|------------|--------------------|------------|--------|------------|----------|----------|--------------------|--------------------|--------------------|--------------------|------------|--------------------|------------|--------------------|--------------------|--------------------|------------|--------------------|------|------------|------------|---------|------------|------------|------------|-----------|----------------|------------|
| SUMMAKIES | ID                   | FUT2_HUMAN         | FUT2_PIG | FUT2_BOVIN        | FUT2_RABIT | FUT2_MOUSE | FUT1_RAT           | FUT1_RABIT | - 1    | FUT1_HUMAN | FUT1_PIG | FUT2_RAT | YKQ7_CAEEL         | FUT8_PIG           | FUT8_HUMAN         | FUT8_MOUSE         | YGPO_YEAST | ALN_RANCA          | MIAA_RALSO | CTPC_MYCTU         | S6A4_CAVPO         | CBPA_ANOGA         | FHUB_ECOLI | GLK_NEIMA          | - 1  | FUT8_BOVIN | ATC6_SCHPO | LPH_RAT | NOEA_RHIME | FUT6_ARATH | S6A4_MOUSE | S6A4_RAT  |                | BCSA_SALTY |
|           | DB                   | -                  | Н        | Н                 | Н          | Н          | Н                  |            | Н      | Н          | -        | Н        | 7                  | 7                  | Т                  | Н                  | Н          | -                  | Н          | Н                  | Н                  | ٦                  | Н          | Н                  | Н    | Н          | гH         | Н       | Н          | Н          | Н          |           | <del>- 1</del> | Н          |
|           | Length               | 343                | 340      | 344               | 354        | 368        | 376                | 373        | 376    | 365        | 365      | 159      | 365                | 575                | 575                | 575                | 1489       | 484                | 323        | 718                | 630                | 433                | 660        | 328                | 1048 | 575        | 1211       |         | 476        | 537        | 630        | 630       | 1279           | 874        |
| ď         | $^{\rm ry}_{\rm ch}$ | 16                 | N        | Н                 | ₹          | 0          | 6                  | g          | 58.6   | 8          | æ        | 3,       |                    |                    |                    | 4.9                | 4.8        | 4.7                | 4.6        | 4.6                | 4.6                | 4.5                | 4.5        | 4.5                | 4.5  | 4.4        | 4.4        | 4.4     | 4.4        | 4.4        | 4.4        | 4.4       | 4.4            | 4 . 4      |
|           | Score                | ; 4                | 152      | 51                | 375.       | 299.       | 100.               | 093.       | 1083.5 | 080        | 079.     | 623      | 155                | 92                 | 06                 | 06                 | 89         | 86.5               | 85         | 85                 | 84.5               | 84                 | 83.5       | 83                 | 82.5 | 82         | 82         | 82      | $\vdash$   | Н          | Н          | 81.5      | Н              | 0          |
|           | Result<br>No.        | 1                  | 7        | m                 | 4          | Ŋ          | 9                  | 7          | 80     | σ          | 10       | 11       | 12                 | 13                 | 14                 | 15                 | 16         | 17                 | 18         | 19                 | 20                 | 21                 | 22         | 23                 | 24   | 25         | 26         | 27      | 28         | 29         | 30         | 31        | 32             | 33         |

| Q92448 pichia past | Q56855 yersinia en | 095897 homo sapien | Q9xqv2 heterocapsa | P87078 candida alb | P40601 photorhabdu | P28820 bacillus su | Q01365 barley yell | O06458 thermus the | P56786 arabidopsis | Pl3887 ross river | Q47266 erwinia chr |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| K6P1_PICPA         | FES_YEREN          | NOE2_HUMAN         | PSAB_HETTR         | TOP2_CANAL         | LIP1_PHOLU         | PABB_BACSU         | POL2_BAYMG         | TRES THETH         | YCF2_ARATH         | POLN_RRVN         | HMPA_ERWCH         |
| Н                  | Н                  | П                  | Н                  | Н                  | <b>,</b>           | Н                  | Н                  | -1                 | Н                  | Н                 | ٦                  |
| 066                | 353                | 454                | 776                | 1461               | 645                | 470                | 890                | 963                | 2294               | 2479              | 395                |
| 4.3                | 4.3                | 4.3                | 4.3                | 4.3                | 4.2                | 4.2                | 4.2                | 4.2                | 4.2                | 4.2               | 4.2                |
| 80                 | 79.5               | 7.9                | 7.9                | 29                 | 78.5               | 7.8                | 7.8                | 7.8                | 7.8                | 7.8               | 77.5               |
| 34                 | 35                 | 36                 | 37                 | . ee               | ó                  | 40                 | 4.1                | 4.2                | 4.3                | 44                | 45                 |

## ALIGNMENTS

```
Σ
  FUT2_PIG
  RESULT 2
  FUT2_PIG
                                    ŏ
  g
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   ..
   SHORT ISOPORM.

FOR SHORT ISOPORM.

CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

Y-IN XHOSA POPULATION).

/FILd=VAR_003422.

/FILd=VAR_003423.
  61 RGMWIINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120
  181 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF 240
   121 RIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWIFYHHLRQEILQEFTLHDHVREBAQ 180
   VVISNGMANCRENIDISHGDVVFAGDGIEGSPAKDFALLIQCNHTIMIIGIFGIRAAYLI 300
                                       ALTERNATIVE PRODUCTS: TWO PORMS ARE PRODUCED BY THE USE OF ALTERNATIVE INTITIATION CODONS IN THE SAME READING FRAME.

TISSUE SPECIFICITY: SMALL INTESTINE, COLON AND LUNG.

MISCELLANDOUS: THERE ARE TWO GENES (FUTI AND FUT2) WHICH ENCODE GALACTOSIDE 2-1-FUCGSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERMAL ORIGIN RESPECTIVELY.

SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
  Gaps
   9
  9
PATHWAY: Glycosylation.
SUBCELDIAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
   2,
   d
  MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL
   Polymorphism.
43 GALACTOSIDE 2-L-FUCOSYLTRANSFERASE
   LONG ISOFORM.
GALACTOSIDE 2-L-FUCOSYLITRANSFERASE
  MIM; 182100; -.
InterPro; IPR002516; GT_11.
Pfam; PF01531; G1yco_transf_11; 1.
Transferase; G1ycosyltransferase; G1ycoprotein; Transmembrane; Signal-anchor; G04g1 stack; Alternative initiation;
Blood group antigen; Polymorphism.
  1;
   99.1%; Score 1832.5; DB 1; Length 343; 99.7%; Pred. No. 9.2e-150;
   -> F (IN JAPANESE SEJ ALLELE;
  /FIIG-VAR_003424.
D -> N (IN XHOSA POPULATION)
/FIId-VAR_003425.
12066D9CF175E13A CRC64;
  Indels
  ·
0
   0; Mismatches
   SECRETOR
   39017 MW;
   EMBL; U17894; AAC24453.1; -. EMBL; D89327; BAA13944.1; -. EMBL; D87942; BAA21684.1; -.
  343; Conservative
  343
  343
  12
14
14
188
188
308
25
25
  172
   138
   343 AA;
   Similarity
  12
   172
   15
29
188
282
308
25
   138
  DOMAIN
TRANSMEM
   CARBOHYD
CARBOHYD
  INIT_MET
   SEQUENCE
   CARBOHYD
   Query Match
  DOMAIN
  VARIANT
   VARIANT
  VARIANT
   VARIANT
  Local
   CHAIN
  CHAIN
  Matches
  61
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   010982; 029044; 019100;
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)Fr 2)
240 VVTSNGMAMCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT 299
   CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
  MEDINESPERSON N.A.
MEDINESPERSON N.A.
MEDINESPERSON N.A.
MEDINESPERSON N.A.
MEDIATION E., Fries R., Voegeli P., Masabanda J., Wigger G.,
Stricker C., Neuenschwander S., Bertschinger H.U., Stranzinger G.;
"Two alpha(1,2) fucosyltransferase genes on porcine chromosome 6q11
are closely linked to the blood group inhibitor (S) and Escherichia
coli F18 receptor (ECRIBR) loci.";
Mamm. Genome 8:736-741(1997).
  Euteleostomi;
Sus.
  Cohney S., Mouhtouris E., McKenzie I.F.C., Sandrin M.S.; "Molecular cloning and characterization of the pig secretor type alpha(1,2)fucosyltransferase."; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
   Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
   Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
  300 GGDTIXLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLKH 343
   3C1 GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Sulna; Suidae;
  or send an email to license@isb-sib.ch).
   SEQUENCE OF 69-80; 119-133 AND 316-334
  PRT;
   EMBL; U70881; AAB81883.1; ~.
  SEQUENCE OF 69-334 FROM N.A.
  EMBL; AF027304; AAC09170.1;
EMBL; X99621; CAA67932.1; -.
   Signal-anchor.
   InterPro; IPR002516; GT_11
   STANDARD;
   (Fucosyltransferase 2)
   [2]
SEQUENCE FROM N.A.
   Sus scrofa (Pig).
   NCBI_TaxID=9823;
   Golgi stack;
DOMAIN
   TRANSMEM
  PAGE STATE S
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IPR002516; GT_11
  NCBI_TaxID=9986;
   TISSUE=Brain;
   FUT2_RABIT
Q10983;
  CARBOHYD
   TRANSMEM
  CARBOHYD
  CARBOHYD
  CARBOHYD
   SEQUENCE
   DOMAIN
   FUT2_RABIT
  300
   RESULT 4
   ID DETAIL DE LE PROPERTIE LE PR
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   g
  δ
   qq
   δλ
      g
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   2,
  FUTZ_BOVIN STANDARD, PRT; 344 AA.

028113;
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
   240
   180
  241 VVTSNGMAWCRENIDISHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT 300
   237 VVSSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTVMTIGTFGIWAAYLA 296
  61 RGMWTINAIGRLGNQMGEYATLYALAKWNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120
  Gaps
   57
   1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL 60
  Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
-!- PATHWAY: Glycosylation.
-!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
  121 RIPWQNYHLNDWMEEEYRHIPPGEYVRFIGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ
  181 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF
                        LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

R-JHKED (GLCNAC. .) (POTENTIAL).

R-H (IN REF. 3).
  . 7
  Length 340;
   Indels
   -> H (IN REF. 3).
0629F1C04FC206AD CRC64;
   GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  Score 1528; DB 1;
Pred. No. 1.1e-123;
   24; Mismatches
             (POTENTIAL)
  38987 MW;
  82.6%;
82.0%;
   EMBL; X99620; CAA67931.1; -
   Matches 282; Conservative
  (Fucosyltransferase 2).
                               340
185
251
279
305
158
   30s taurus (Bovine).
                             29
185
185
251
279
305
340 AA;
  SEQUENCE FROM N.A.
   Similarity
   NCBI_TaxID=9913;
  Petit J.M.;
Submitted (
                               DOMAIN
CARBOHYD
CARBOHYD
  CARBOHYD
   Query Match
Best Local S
  SEQUENCE
  CARBOHYD
  FUT2_BOVIN
  301
   RESULT
   g
   QQ
  QΩ
   Qγ
   qq
  δ
  Dp
  δλ
   ŏ
  δy
             FT
FT
FT
FT
FT
SQ
```

```
179
   240 FVVSSNGMAWCRENINASRGDVVFAGNGNEGSPAKDFALLTOCNHTIMTIGTFGIWAAYL 299
   Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S.;
"Molecular cloning and expression of two types of rabbit betagalactoside alpha 1,2 fucosyltransferase.";
J. Biol. Chem. 270:8844-8850(1995)
J. Biol. Chem. 270:8844-8850(1995)
J. Biol. Chem. 270:8844-8850(1995)
J. Biol. Chem. 270:8844-8850(1995)
J. Biol. Chem. 270:8844-8850(1995)
J. Biol. Chem. 270:8844-8850(1995)
J. Biol. Chem. 270:8844-8850(1995)
SOBSTRAIB FOR THE FINAL STEP IN THE SOLUBLE A'AND B ANTIGEN SYMPHESIS BUT EXHIBIT DIFFERENT KM VALUES.
  60 LRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATA 119
   SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
  1 MLVVQMPFSFPNAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGP-SQ 59
   09
  Gaps
  01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
18-JUN-2002 (Secretor blood grandstare)
18-JUN-2002 (Secretor blood grandstare)
18-JUN-2002 (Secretor blood grandstare)
18-JUN-2002 (Secretor blood grandstare)
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18-JUN-2002 (Secretor blood grandstare)
18-JUN-2002 (Secretor blood grandstare)
18-JUN-2002 (Secretor blood grandstare)
18-JUN-2002 (Secre
  120 SRIPWQNYHLNDWMEEEYRHIPPGEYVRFIGYPCSWTFYHHLRQEILQEFTLHDHVREEA
   180 QKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLI
   240 FVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYL
  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidaè; Oryctolagus.
   CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP
  (LOMBUAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
  ..
InterPro; IPR002516; GT 11.
Pfam; PF01531; Glyco.mnsf_11; 1.
Transferase, Glycosyltransf_11; 6.
  DB 1; Length 344;
  Indels
  TGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  300 AGGETIYLANYTLPDSPFLKIFKPEAAFLPKWIGIPADLSPLLKH 344
  CYTOPLASMIC (POTENTIAL)
  45;
  Pred. No. 4.1e-122;
  14; Mismatches
  81.6%; Score 1510;
82.3%; Pred. No. 4.
   (POTENTIAL)
  MEDLINE=95238380; PubMed=7721792;
   01-0CT-1996 (Rel. 34, Created)
  39320 MW;
  Golgi stack; Signal-anchor.
DOMAIN 1 7
  Query Match
Best Local Similarity 82.3
Matches 284; Conservative
   STANDARD;
  (Fucosyltransferase 2)
FUT2 OR SEC1 OR RFT-II
  28
  344
189
255
283
309
  29
189
255
283
309
344 AA;
  SEQUENCE FROM N.A.
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  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
   3;
  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-rfucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
FUT2 OR SEC1.
  251
  140
   132 WMEEEYRHIPPGEYVRFIGYPCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRGLQVNGS 191
  72 LGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLND 131
   200 RPSTFVGVHVRRGDYVRVMPQVWKGVVADRGYLEQALDWFRAPTAPPVFVVTSNGMAWCR 259
  SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
   Gaps
   14 HFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL--RGMWTINAIGR 71
             PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
TISSUE SPECIFICITY: SALLVARY AND LACTATING MAMMARY GLANDS.
   192 RPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCR
   ENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYT
   -1- TISSUE SPECIFICITY: SALIVARY AND LACTALING MAGNETY.
-1- MISCELLANEOUS: THERE ARE THREE GENES (FUIL, FUIZ AND FUI3) WHI
ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE IN RABBIT. THEY ARE
  UMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

1 IE2B831F9DA6CCB4 CRC64;
  EMBL, X80225; CAA56512.1; -.
Interpro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
  DB 1; Length 354;
   EXPRESSED IN A TISSUE-SPECIFIC. MANNER.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11
   41; Indels
  CYTOPLASMIC (POTENTIAL)
   ; Score 1375.5; DB 1; Pred. No. 1.4e-110; 26; Mismatches 41;
 alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
   368
   312 LPDSPFLKIFKPEAAFLPEWTGIAADLSPLL 342
   320 APDSPFHLVFKPEAAFLPEWVGITANMGRAL 350
   (POTENTIAL)
   40035 MW;
   74.48;
76.48;
   Golgi stack.
   Best_Local Similarity 76.43
Matches 253; Conservative
   STANDARD;
  Mus musculus (Mouse)
   44
197
291
317
354 AA;
   Signal-anchor;
DOMAIN
  FUT2_MOUSE
P97353;
   CARBOHYD
CARBOHYD
  TRANSMEM
  CARBOHYD
  SEQUENCE
   Match
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   245
  246 GMAWCRENIDISHGDVVFAGDGIEGSPAKDFALLIQCNHIIMTIGTFGIWAAYLTGGDTI 305
  INAIGREGNOMGEYATEYALAKMNGRPAFIPAOMHSTLAPIFRITEPVEHSATASRIPWO 125
  CYTOPLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
   15; Gaps
  11 PMAHFILF--VFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQ---LRGMWT 65
  22 PLSTFYLFFVIFVVSTIFHCHRRLGLVPAPW------ASPSLVVFPPRHMPREGMFT 72
   13 IRVKGRIGNQMGEYATLFALARMNGRLAFIFASMHSTLAPIFRISLPVLHSDTAKRIFWQ
  Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S.;
Molecular clohing and expression of a mouse GDP-L-Fucose: beta-D-
galactoside 2-alpha-L-Fucosyltransferase.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
   NYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRG
  LQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSN
   (POIENTAL).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
: Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi.
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
  InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
  70.2%; Score 1299.5; DB 1; Length 368; 73.6%; Pred. No. 4.8e-104;
   GALACTOSIDE 2-L-FUCOSYLTRANSFERASE.
   SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=ICR; TISSUE-Gastrointestinal tract; Lin B., Hayashi Y., Saito M., Sakakihara Y., Yanagisawa M., Iwamori M.;
   Indels
  N-LINKED (GLCNAC. . .) (Po
4093E853EB37303B CRC64;
  43;
  Best Local Similarity 73.6%; Pred. No. 4.8e-
Matches 245; Conservative 30; Mismatches
   (POTENTIAL)
  EMBL; Y09882; CAA71008.1; -. EMBL; AF113532; AAD25351.1; -. MGD; MGI:109374; Fut2.
   41464 MW;
   Signal-anchor; Golgi stack.
     Eukaryota; Metazoa;
   42
195
289
315
368 AA;
   SEQUENCE FROM N.A.
                              Mammalia; Eutheri
NCBI_TaxID=10090;
  STRAIN-ICR;
   DOMAIN
CARBOHYD
  CARBOHYD
SEQUENCE
   TRANSMEM
  CARBOHYD
  Query Match
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Best Local Similarity
   FUT1_RABIT
                 Matches
  37
  9
   113
   155
  172
  Db
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  01-02T-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
15-JUL-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
  SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 252 DMAWCRKSITASRGDVAFAGNGLQGSPAKDIALLMQCNHTVITLGTFGIWAAYLTGGDTV 311
   SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN, MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
MISCELLARBOUS: THERE ARE TWO GENES (FUTL AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
  (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
   EMBL; L26009; AAB41514.1; -.
InterPro; IPRO02316; G3-11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
  LUMENAL, CATALYTIC (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENT
N-LINKED (GLCNAC. .) (POTENT
N-LINKED (GLCNAC. .) (POTENT
   'Two distinct rat GDP-L-fucose:b-D-galactoside 2-alpha-L-
  fucosyltransferase genes.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
   C350C737C758B7F8 CRC64;
   CYTOPLASMIC (POTENTIAL).
   376 AA
                                    306 YLANYTLPDSPFLKIFKPEAAFLPEWTGIAADL 338
   312 YLANFTQPNSPFHTVFKPEAAYLPEWVGIAADL 344
   (POTENTIAL)
   Soejima M., Wang B., Koda Y., Kimura H.;
   PRT;
  MEDLINE=94280382; PubMed=8010942;
  EMBL; AB015637; BAA31130.1; -.
  EMBL; AB006137; BAA21741.1; -.
  42416 MW;
   SEQUENCE OF 169-310 FROM N.A.
   stack.
   STANDARD;
  Rattus norvegicus (Rat)
   64
302
   (Fucosyltransferase 1).
   Golgi
  rissuE=Colon cancer;
  64
302
328
376 AA;
  SECUENCE FROM N.A.
  NCBI_TaxID=10116;
  Signal-anchor;
DOMAIN
  FUT1 OR FTA.
  CARBOHYD
   FUT1_RAT
Q10980;
  PRANSMEM
   CARBOHYD
   CARBOHYD
   DOMAIN
  RESULT
   g
  QΫ
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Length 376;

DB 1;

Score 1100.5;

59.5%;

Query Match

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                                  4;
   olocar-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
Fruch OP Press 1).
   VWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSP 272
  WTFYHHLRQZILQEFTLHDHVREEAQKFLRGLQVN--GSRPGTFVGVHVRRGDYVHVMPK 212
   AKDFALLIQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWT 332
   AMVCLP--YPSNASSGSPSCPEQSLLSGTWTITPGGRFGNOMGQYATLLALAQLNGRRAF 112
  IPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLNDWMEBEYRHIPPGEYVRFTGYPCS 154
   292 GKDFALLTQCNHTIMTIGTFGFWAAXLAGGDTVXLANFTLPDSBFLKIFRFKAAFLPEWV 351
                                  Gaps
   -i- TISSUE SPECIFICITY: BRAIN.
-i- MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLIFRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERNAL OR ENDODERNAL ORIGIN RESPECTIVELY.
-i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
   -!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
   AMWELPVQIPVLASTSKALGPSQ---LRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAF
  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
  = GDP
   MEDLINE=95238380; pubMed=7721792;

METORINE S., Kusunoki S., Kanazawa I., Tsuji S.;

Molecular cloning and expression of two types of rabbit beta-

galactoside alpha 1,2-fucosyltransferase.";

J. Biol. Chem. 270:8844-8850(1995).

-!-CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = Gl

alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                  Indels
               Pred. No. 5.7e-87;
; Mismatches 59;
   PRT;
67.0%; Kin
  InterPro; IPR002516; GT_11.
   EMBL; X80226; CAA56513.1;
                                      Conservative
   STANDARD;
   352 GINADLSPL 360
   333 GIAADLSPL 341
   SEQUENCE FROM N.A.
  NCBI_TaxID=9986;
   FUT1_RABIT
Q10979;
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FUT1_HUMAN P19526;
  CARBOHYD
SEQUENCE
  TRANSMEM
   CARBOHYD
  CARBOHYD
  Query Match
  DOMAIN
   DOMAIN
   FUT1_HUMAN
   163
  181
   222
  ID DE POLICE CONTRACTOR CONTRACTO
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  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNC-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
   SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERRAE OF GOLGI.
TISSUE SPECIFICITY: IN THE ADULT, HIGHLY EXPRESSED IN PANCREAS, TESTIS AND EPIDIDYMIS AND TO A LESSER EXTENT IN THYMUS, LUNG, STOMACH, SMALL INTESTINE, COLON, SPLEEN AND UTERUS. NOT EXPRESSED
   296
   STLAPIFRITLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHH 160
  LRQEILQEFTLHDHVREEAQKFLRGLQV--NGSRPGTFVGVHVRRGDYVHVMPKVWKGVV 218
  279 LIQCHHILMTIGTFGIWAAYLIGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADL 338
  41 LPVQIPVLASTSKALGPSQLRGMWTINAIGRLGNQNGEXATLYALAKMNGRPAFIPAQMH 100
  58 LPVTSPASNASSCAGRPAAPSGIWTIHPDGRFGNOMGQYATLLALAQLNGRRAFILPAMH 117
   CYTOPLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
  Gaps
  219 ADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFAL
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
   Domino S.E., Hiraiwa N., Lowe J.B.;
"Molecular cloning, chromosomal assignment and tissue-specific expression of a murine alpha(1,2)fucosyltransferase expressed in thymic and epididymal epithelial cells.";
Blochem. J. 327:105-115(1997)
- :- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
  UMBUNL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
0A47A1786231525C CRC64;
   3;
Pfam; PF01531; Glyco_transf=11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack.

CYTOPLASMIC (POTENTIAL).
TRANSMEM 13 29 SIGNAL-ANCHOR (TYPE-II MEMBRANE P)
   DB 1; Length 373;
  59; Indels
  Match . 59.1%; Score 1093.5; DB . Local Similarity 67.0%; Pred. No. 2.2e-86; Les 203; Conservative 38; Mismatches 59.
   376 AA
  (POTENTIAL).
   PRT;
   MEDLINE=97454449; PubMed=9355741;
  42098 MW;
   PATHWAY: Glycosylation.
   STANDARD;
  373
66
301
327
  (Fucosyltransferase 1).
  Mus musculus (Mouse)
  30
66
301
327
373 AA;
  SEQUENCE FROM N.A. STRAIN=NIH Swiss;
   NCBI_TaxID=10090;
  339 SPL 341
   SPV 359
   FUT1_MOUSE
009160;
  DOMAIN
CARBOHYD
   CARBOHYD
CARBOHYD
SEQUENCE
   Query Match
   FUT1_MOUSE
   161
   101
  Dp
  qq
  g
   g
   δy
   q
  ŏ
   pp
    KKW
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   3;
  SIGNAL-ANCHON (TYPE-II MEMBRANE PROTEIN).
LUMEDAL, CATALYIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
  01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JW-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1)
(Fucosyltransferase 1) (Alpha(1,2)FT 1)
  241 AYLQQAMDWFRARHKDPIFVVTSNGMKWCLENIDTSHGDVVFAGNGQEGTPGKDFALLIQ 300
  46 PVLASTSKALGPSQ----LRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHST 102
   62 PLQTSNGSPSCPEQSSSLSGTWTITPGGRFGNQMGQYATLLALAQLNGRQAFIQPEMHAA 121
   103 LAPIFRITLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLR 162
  EQIRREFTLHNHLREGAQYLLSGLRIGPASPAHTFVGVHVRRGDYLEVMPNRWKGVVGDR 240
   RYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQ 281
   282 CNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPL 341
   SEQUENCE FROM N.A.
MEDDLINE-90370848; Pubmed=2118655;
Larsen R.D., Ernst L.K., Nair R.P., Lowe J.B.; ...,
"Molecular cloning, sequence, and expression of a human GDP-L-
fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase cDNA that can
  Gaps
IN BRAIN, HEART, SKELETAL MUSCLE, KIDNEY, LIVER AND BONE MARROW -!- MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
  QEILQEFTLHDHVREEAQKFLRGLQVNGSRPG-TFVGVHVRRGDYVHVMPKVWKGVVADR
   Euteleostomi;
  EMBL; U90553; AAC53492.1; ...
MGD; MGI:109375; Fut1.
InterPro; IPR002516; GT.11.
Pfam; PF01531; GlycoxoLransf_11; 1.
Transferase; GlycoxyLtransf_11; 1.
Signal-anchor; Golgi stack.
   58.6%; Score 1083.5; DB 1; Length 376; 67.0%; Pred. No. 1.6e-85;
  Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
   61; Indels
   N-LINKED (GLCNAC. . .) (PC
21F1D24CFE204106 CRC64;
  CYTOPLASMIC (POTENTIAL)
   33; Mismatches
  365 AA
  PRT;
   67 N-
302 N-
328 N-
42255 MW;
   Chordata; (
Primates; (
   Matches 201; Conservative
  STANDARD;
   Homo sapiens (Human)
  Eukaryota; Metazoa;
Mammalia; Eutheria;
   9
27
67
302
328
376 AA;
  Best Local Similarity
  NCBI_TaxID=9606;
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RESULT 10
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  ACARDO STATE
   H
  WEDLINE=97445117; PubMed=9299444;
MEDLINE=97445117; PubMed=9299444;
Model Y., Soejima M., Johnson P.H., Smart E., Kimura H.;
Model Y., Soejima M., Johnson P.H., Smart E., Kimura H.;
Model Y., Soejima M., Johnson P.H., Smart E., Kimura H.;
Indian Bombay phenotype at ABO blood group system.";
Biochem. Biophys. Res. Commun. 238:21-25(1997).
-!- FUNCTION: CREATES A SOLUBLE PRECURSOR OLIGOSACCHARIDE FUG-ALPHA
((1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN ESSENTIAL
SUBSTRATE FOR THE FINAL STEP IN THE SOLUBLE A AND B ANTIGEN
SYNTHESIS PATHAMAY. H AND SE BIZYMES FUGOSYLATE THE SAME ACCEPTOR
SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.
-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyi-R = GDP +
AD THE STEP IN THE STEP IN THE SOLUBLE A AND B ANTIGEN
SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.
-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyi-R = GDP +
AD THE STEP IN THE STEP 
  BOMBAY BLOOD GROUP.

--- MISCELLANBOOS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERWAL OR ENDODERMAL ORIGIN RESPECTIVELY.

--- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
   -!- POLYMORPHISM: NONFUNCTIONAL MUTANT OF FUT1 ARE THE CAUSE OF THE
   PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI.
   Lowe J.B.; "Molecular basis for H blood group deficiency in Bombay (Oh) and
  MEDLINE-94286534; PubMed-7912436;
Kelly R.J., Ernst L.K., Larsen R.D., Bryant J.G., Robinson J.S.,
  Wagner F.F., Flegel W.A.; "Polymorphism of the hallele and the population frequency of sporadic nonfunctional alleles."; Fransfusion 37:284-290(1997).
   W -> C (IN BOMBAX H-).

/FIId=VAR_003418.
L -> R (IN BOMBAX H-).

/FIId=VAR_009709.
V -> E (IN BOMBAX H-).
   /FTId=VAR_003417.
L -> H (IN PARA-BOMBAY).
/FTId=VAR_009708.
        form the H blood group antigen.";
Proc. Natl. Acad. Sci. U.S.A. 87:6674-6678(1990).
  para-Bombay individuals.";
Proc. Natl. Acad. Sci. U.S.A. 91:5843-5847(1994)
   SEQUENCE FROM N.A., AND VARIANT ALLELES MEDLINE-97240210; Pubmed-9122901;
  EMBL; M35531; AAA52639.1; -.
EMBL; Z69587; CAA93435.1; -.
PIR; A36047; A36047.
  Genew; HGNC:4012; FUT1.
   171
  242
  242
   259
   171
   VARIANT HIS-164
   'ARIANT
  VARIANT
   VARIANT
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.,
   (GDP-L-fucose:beta-
  189
  12 MAHFILEVETVSTIFHVQQR-----LAKIQAMWELPVQIPVL-----ASTSK 53
   11 LAFLLVCVLSVIPFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
   Gaps
  MEDINE=97468270; PubMed=9321466; Masabanda J., Wigger G., Meijerink E., Frisa R., Voegeli P., Masabanda J., Wigger G., Stricker C., Neuenschwander S., Bertschinger H.U., Stranzinger G.; "Two alpha(1,2) fucosyltransferase genes on porcine chromosome 6q11 are closely linked to the blood group inhibitor (S) and Escherichia accoli F18 receptor (ECRIBA) loci."; Mamm. Genome 8:736-741(1997).
   TISSUE=Small intestine;
Meijerink E., Neuenschwander S., Fries R., Dinter A.,
Bertschinger H.U., Stranzinger G., Voegeli P.;
"Expression and activity of porcine alpha(1,2)fucosyltransferases
  54 ALGPSQLRGNWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV
  114 LHSATASRIPWQNYHLNDWMEETRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD
  HVREEAQKFLRGLQV--NGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWF
  RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGT
   Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartlodactyla; Suina; Suidae; Sus.
  21;
  DB 1; Length 365;
  01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
621actoside 2-L-itucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fu
D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT
   FGIWAAYLTGGDTIXLANYILPDSPFLKIFKPEAAFLPEWTGIAADLSPL 341
   Cohney S., Mouhtouris E., McKenzie I.F., Sandrin M.S.; "Molecular cloning of the gene coding for pig alphal-->2
   Indels
  4F4442EC375C9D9E CRC64;
  SEQUENCE FROM N.A., AND VARIANTS THR-103 AND GLN-286.
   /FTIG=VAR_003420.
W -> C (IN BOMBAY H-).
/FTIG=VAR_003421.
/FTId=VAR_003419.
A -> V (IN BOMBAY H-).
/FTId=VAR_003420.
   79:
   8e-85;
   365 AA
  Score 1080.5;
Pred. No. 2.8e
   41; Mismatches
   PRT;
  MEDLINE=96217559; PubMed=8613146;
   Lmmunogenetics 44:76-79(1996).
  MM:
  58.4%;
   41251
   Matches 209; Conservative
   STANDARD;
                                315
   349
  (Fucosyltransferase 1)
  fucosyltransferase.
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   365 AA;
   Similarity
   NCBI_TaxID=9823;
  029043; 019101;
01-NOV-1997 (Rel
16-OCT-2001 (Rel
                                315
   349
   FUT1_PIG
  SEQUENCE
   Query Match
                                VARIANT
   VARIANT
   Sest Local
  232
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      S
   CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
   271
   51 PVAIFCLAGTPVHFNASDSCPKHPASLSGTWTIYPDGRFGNOMGOYATLLALAOLNGROA 110
   153
  211
  331
   11; Gaps
   42 PVQIPVLAST-----SKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPA 93
  MISCELLANBOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER.
   O status and susceptibility
determine erythrocyte antigen precursor o status and susceptibility Escherichia coli Fi8 colonization in the small intestine.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: GDP-1-fucose + beta-D-galactosyl-R = GDP +
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
-:- PATHWAY: Glycosylation.
-:- PATHWAY: Glycosylation.
-:- SUBCELLULAR LOCASILION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
  94 FIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPC
   SWIFYHHURQEILQEFILHDHVREEAQKFLRGLQV - - NGSRPGIFVGVHVRRGDYVHVMP
   212 KVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGS
  PAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEW
  EMBL, U70883; AAB81884.1; -.
EMBL, AF136896; AAF59833.1; -.
Interpro, IPRO02516; Gr_11.
Pfam, PF01531; Glyco_transf.11; 1.
Transferase, Glycoprotein; Transmembrane; Signal-anchor; Golgi stack; Polymorphism.
   58.4%; Score 1079.5; DB 1; Length 365; 65.5%; Pred. No. 3.4e-85;
  SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
   66; Indels
  -> Q.
-> F (IN REF. 1).
DAFCE77E89A29D75 CRC64;
   30; Mismatches
  -> I
   41106 MW;
   EMBL; L50534; AAB02984.1; -.
   Matches 203; Conservative
  28
365
65
301
327
103
286
  77
365 AA;
  TGIAADLSPL 341
  350 VGINADLSPL 359
   Similarity
   CARBOHYD
  TRANSMEM
   CARBOHYD
  Query Match
Best Local (
   SEQUENCE
   CONFLICT
   VARIANT
  VARIANT
   DOMAIN
  DOMAIN
  154
   170
  230
  272
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   Piau J.-P., Labarriere N., Dabouis G., Denis M.G.;

Evidence for two distinct alpha(1,2) fucosyltransferase genes

"Evidence for two distinct alpha(1,2) fucosyltransferase genes

differentially expressed throughout the rat colon.";

Elochem. J. 30.623-626(1994).

C. I. FUNCION: CREATES A MEMBRANE-ASSOCIATED PRECURSOR OLIGOSACCHARIDE

FUC-ALPHA((1,2))GALBETA-) CALLED THE H ANTIGEN WHICH IS AN

ESSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE MEMBRANE-ASSOCIATED

C. AND B ANTIGEN SYNTHESIS PATHWAY. HAND SE ENZYMES FUCOSYLATE

THE SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.

C. I. CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +

alpha-L-fucosyl-1,2-beta-D-galactosyl-R.

C. I. PATHWAY: Glycosylation.

C. I. SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND

C. I. SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND

FORM IN TRANS CLYSTERNAE OF GOLGI (PY SIMILARITY).
   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae: Rattus.
NCBI_TaxID=10116;
  Gaps
   67
   -!- MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A IISSUE-SPECIFIC MANNER.
   Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (Secretor blood group alpha-2-fucosyltransferase) (GDP-L-fucoss:beta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2) (Fucosyltransferase 2) (Fragment).
   2 VWKGVVADRGYLEKALDMFRARXSSPVFVVTSNGMAMCRENINASRGDGVFAGNGIEGSP
  273 AKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWT
  213 VWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSP
  ..
O
  98 98 N-LINKED (GLCNAC. . .) (POIENTIAL)
159 AA; 17250 MW; 14DECEB7C2E6384A CRC64;
  Interpro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
  Length 159;
  -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY
   9; Indels
  Score 623; DB 1;
Pred. No. 1.7e-46;
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
   AA.
   Mismatches
   PRT;
   MEDLINE=94280382; PubMed=8010942;
   YKQ7_CAEEL STANDARD; F P34302; 01-FEB-1994 (Rel. 28, Created)
   33.7%;
Similarity 88.5%;
16; Conservative (
   EMBL; L26010; AAB41515.1;
  Rattus norvegicus (Rat).
   333 GIAADLSPLLK 343
   GIPADLSPLLK 132
  OR SEC1 OR FIB.
   SEQUENCE FROM N.A.
  Ma.
Local s.
116;
   Golgi stack
  STRAIN=BDIX
  CARBOHYD
  SEQUENCE
  Query Match
   RESULT 12
YKQ7_CAEEL
   122
   Matches
  AC DI
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159 AA.

PRT;

FUT2\_RAT STANDARD; F Q10984; 01-0CT-1996 (Rel. 34, Created)

DA E

RESULT 11 FUT2\_RAT

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  21;
  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
WILSON R., Alnscough R., Anderson K., Baynes C., Berks M.,
EDITION R., Alnscough R., Connell M., Copsey T., Cooper J., Coulson A.,
Carkton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Johnston L., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sins M., Smmldon N., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Meg J., Ihomas K., Vaudin M., Vaughan K.,
Matesfato R., Watson A., Weinstock L., Wilkinson-Sproat J.,
   268
  69 ASTARLANHIFELVSVYGMAKSLNRKPAIFVEDSKYNLLITGVRKVLPGLLDEFQIFEYP 128
   115 -HSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD 173
   223
   EGSPAKDFALL-TQCNHTIMTI--GTFGIWAAYLTGGDTIYLANY-TLPDSPFLK-IFKP 323
   67 NAIGRIGNOMGEYATLYALAK-MNGRPA-FIPAQMHSTLAPIFRITLPVL------ 114
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase C06B1.7 in chromosome III (EC 2.-.-).
  Gaps
   LFVFTVST1FHVQQRLAKIQAMWELPVQ1PVLAS------TSKALGPSQLRGMWT--I 66
   10 LLCVLVVVLFFINNQFVQ-RTTWSRGLRSPPLDSRIFQEKSEIERSTLPPIPKGFLSSKL 68
  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
  ن
   129 VHN-KATKVPLSEKCCIFDNPDKFNNI-SSEYLHLTGH----FY-----QSWKYFD
   174 HVREEAQKFLRGL----QVNGSRPGTFVG---VHVRRGDYV---HVMPKVWKGVVADRRY
   174 KYKEKVOSFVKPAIDFSPLPNSDSSNFISRICIHIRRIDFVDGQHHSSNV----SF
   24 LOOALDWFRAR----YSSLIFVVTSN-----GMAWCRENIDTSHGDVVFAGDGI
   '2.2 Mb of contiguous nucleotide sequence from chromosome III of
  80;
   Waterston R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
  Length 365;
  66; Mismatches 149; Indels
  Wormep; C06E1.7; CE30483.
InterPro; IPR002516; GT_11.
Pfam; PF01531; G1yco_transf_11; 1.
Hypothetical protein; Transferase; G1ycosyltransferase.
SEQUENCE 365 AA; 41991 MW; B5FBCA363F31977F CRC64;
  DB 1;
   6e-06;
  8.4%; Score 155;
21.1%; Pred. No. 6
   EMBL; L16559; AAA27932.2; -.
   --
--
  Conservative
  Natúre 368:32-38(1994).
  Caenorhabditis elegans
  Best Local Similarity
Matches 79; Conserv
   NCBI_TaxID=6239;
   Wohldman P.;
  REVISIONS
  Query Match
   elegans
   269
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   Uozumi N., Yanagidani S., Miyoshi E., Ihara Y., Sakuma T., Gao C.-X., Teshima T., Fujii S., Shiba T., Taniguchi N.;
"Purification and cDNA cloning of porcine brain GDP-L-Fuc:N-acetyl-beta-D-glucosaminide alphal-->fucosyltransferase.";
J. Biol. Chem. 271:27810-77817(1996).
-!- FUNCTION: Catalyzes the addition of fucose in alpha 1-6 linkage to the first Glunac residue, next to the peptide chains in N-glycans.
  SH3-BINDING (POTENTIAL).
IMPORTANT FOR DONOR SUBSTRATE BINDING (BY
SIMILARITY).
   The pH optimum is 7.

-!- CATALYTIC ACTIVITY: GDP-L-fucose + N4-(N-acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(R(1)-alpha-1,6)-beta-D-mannosyl-beta-N-acetyl-1,4-N-acetyl-D-glucosaminyl-1,4-N-acetyl-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(R(1)-alpha-1,6)-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(R(1)-alpha-1,6)-beta-D-glucosaminyl-1,1,4-N-acetyl-D-glucosaminyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-D-Glucosyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-D-Glucosyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-
  PROTEIN)
  15-70N-2002 (Rel. 41, Created)
15-70N-2002 (Rel. 41, Last sequence update)
15-70N-2002 (Rel. 41, Last annotation update)
15-70N-2002 (Rel. 41, Last annotation update)
15-70N-2002 (Rel. 41, Last annotation update)
15-70N-2002 (Rel. 41, Last annotation update)
16-70N-2002 (Rel. 41, Last annotation u
283 ENTPQDDLAYSHYSCDATLITAPSSTFGWWLGYLSKGQAVYYQDIRSTNDVNYKKGVLDP 342
  glucosaminyl)asparagine.

--- PATHWAY: Glycosylation.

--- SUBCELULAR LOCATION: Type II membrane protein. Membrane-bound form in trans cisternae of Golgi (By similarity).

--- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN.

--- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

--- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 23.
  Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
   Transferase; Glycosyltransferase; Transmembrane; Signal-anchor;
Golgi stack; SH3 domain.
   CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
   SEQUENCE FROM N.A., SEQUENCE OF 102-130; 333-344; 402-415 AND 566-575, AND FUNCTION.
   LUMENAL, CATALYTIC (POTENTIAL).
   575 AA
  (POTENTIAL)
  (alpha1-6FucT) (Fucosyltransferase 8).
  PRT;
  MEDLINE=97066976; PubMed=8910378;
   EMBL; D86723; BAA13157.1; -.
   InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
  PRCSITE; PS50002; SH3; 1.
   STANDARD;
   30
  575
563
305
366
   EAAFLPEWTGIAAD 337
   343 DDFFVPSWTSIMLD
   Sus scrofa (Pig).
  10
  31
502
299
365
  NCBL_TaxID=9823;
   566-575, AND
TISSUE=Brain
   TRANSMEM
   FUT8_PIG
   DOMAIN
SITE
SITE
   DOMAIN
  DOMAIN
  RESULT 13
FUT8_PIG
  324
  qq
                q
  ă
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us-10-040-863-11.rsp

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SITE
   Matches
δλ
  qq
   16;
  FUT8_HUMAN STANDARD; PRT; 575 AA.
09BYC5; OBPXC6; OPPZU5; OSPZU6; 000235;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-(1,6)-fucosyltransferase (EC 2.4.1.68) (Glycoprotein 6-alpha-L-fucosyltransferase) (GDP-L-Fucis) (GDP-L-Fuc
   384
  443
   --GEVKDKNVQVVELPIVDSVHPRPPYLPLAVPEDLAD----RLVRVHGDPA--VWWVSQ 330
  HL-----NDWMEEE-----YRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLH 172
  HHVVYCFMIA--YGTQRTLALESHNWRYATGGWETVFRPVSETCTDRSGSS--TGHWS-- 278
   AIGRLGNOMGEYATLYALAKMNGRPAFIPAOMHSTLAPIFRITLPVLHSATASRIPWONY 127
  "Purification and cDNA cloning of GDP-L-Fuc:N-acetyl-beta-D-glucosaminide.alphal-6 fucosyltransferase (alphal-6 FucT) from human gastric cancer MKN45 cells.";
7. Biochem. 121:626-632(1997).
   ς;
   14 HFILFVFTVSTIFHVQQRLAKIQAMWEL-----PVQIPVLASTSKALGPSQLRGMWTIN 67
   Я.
   DHYREEAQKFLRGLQVNGSR-----PGTFVGVHVRRGDYVHVMPK--VW-----
  - HVEEDFQLLARRMQVDKKRVYLAIDDPALLKEAKIKYPSYEFISDNSISWSAGLHNRYI
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
   Sasho
  "A sequence motif involved in the donor substrate binding by alphal, 6-fucosyltransferase: the role of the conserved arginine
   DONOR SUBSTRATE BINDING, AND MUTAGENESIS OF ARG-365 AND ARG-366
  Calileau A., Balanzino L., Candelier J.J., Oriol R., Mollicone "Differential splice variants of human FUT8 embryonic cDNA."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
   78;
   ENSLRGVILDIHFLSQA-DFLVCTFSSQV------CRVAYEIMQALHPD 485
  fanagidani S., Uozumi N., Ihara Y., Miyoshi E., Yamaguchi N.
   Takahashi T., Ikeda Y., Tateishi A., Yamaguchi Y., Ishikawa
   Yameguchi Y., Ikeda Y., Takahashi T., Ihara H., Tanaka T., Oocumi N., Yanagidani S., Inoue S., Fujii J., Taniguchi N.; "Genomic structure and promoter analysis of the human alphal, 6-fucosyltransferase gene (FOTB).";
   ----KGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCR---ENIDTSHGD
  5.0%; Score 92; DB 1; Length 575; 20.5%; Pred. No. 2.6;
  0F199D0BC2018F7B CRC64;
   108;
   SEQUENCE FROM N.A. (ISOFORM 1), AND FUNCTION. MEDLINE=97279058; PubMed=9133635;
   47; Mismatches
  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
   (alphal-6FucT) (Fucosyltransferase 8).
FUT8
  MEDLINE=20229550; PubMed=10764839;
   MEDLINE=20275614; PubMed=10814706;
  SEQUENCE FROM N.A. (ISOFORM 1).
   ycobiology 10:637-643(2000)
  66229 MW;
   Conservative
  Homo sapiens (Human).
  575 AA;
   Similarity
   NCBI_TaxID=9606;
  Taniguchi N.;
  Taniguchi N.
   60;
    SEQUENCE
   Query Match
   Best Local
  225
   68
  128
   215
   Matches
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   IMPORTANT FOR DONOR SUBSTRATE BINDING.
EVKDKNVQVVQELPIVDSLHPRPPYLPLAVPEDLADRLVRVH
   GDPAVWWVS -> TPIMNLLVITLFPGQLDCTIDTQKIHFV
Glycobiology 10:503-510(2000).

-i-FUNCTION: Catalyzes the addition of fucose in alpha 1-6 linkage to the first Glonac residue, next to the peptide chains in N-glycans.
-i-CATALYTIC ACTIVITY: GDP-L-fucose + N4-(N-acety1-beta-D-glucosaminy1-1,2-alpha-D-mannosy1-1,3-(R(1)-alpha-1,6)-beta-D-mannosy1-1,4-N-acety1-D-glucosaminy1)asparagine = GDP - N4-(N-acety1-beta-D-glucosaminy1-1,1-1,1-alpha-D-mannosy1-1,3-(R(1)-alpha-1,6)-beta-D-glucosaminy1-1,2-alpha-D-mannosy1-1,3-(R(1)-alpha-1,6)-beta-D-mannosy1-1,4-(alpha-1,6)-beta-D-mannosy1-1,5-(alpha-1,6)-(alp
   SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
  14 HFILFVFTVS-----TIFHVQQRLAKIQAMWELPVQIPVLASTŞKALGPSQLRGMWTINA 68
   -i- PATHWAY: Glycosylation.
-i- SUBCELJULAR LOCATION: Type II membrane protein. Membrane-bound form in trans cisternee of Golgi (By similarity).
-i- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/retinal; are produced by alternative splicing.
-i- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 23.
   MISSING (IN ISOFORM 2).
R->A, K: COMPLETE LOSS OF ACTIVITY.
R->A, K: DECREASES ACTIVITY TO 3%.
5AE24A93881E18D0 CRC64;
  Transferase; Glycosyltransferase; Transmembrane; Signal-anchor;
   LUMENAL, CATALYTIC (POTENTIAL).
   4.9%; Score 90; DB 1; Length 575; 20.2%; Pred. No. 3.8;
  46; Mismatches 111; Indels
   SH3 domain; Alternative splicing.

1 9 CYTOPLASMIC (POTENTIAL)
  SH3-BINDING (POTENTIAL)
   E (IN ISOFORM 2)
   (POTENTIAL)
  EMBL, AF038281; AAB92372.2; --
EMBL, AF038280; AAB92372.2; --
EMBL, Y17975; CAA76988.1; --
EMBL, Y17976; CAA76988.1; --
EMBL, Y17976; CAA76986.1; --
EMBL, X17978; CAA76986.1; --
EMBL, AB04978; CAA76987.1; --
EMBL, AB049740; BAB40929.2; --
EMBL, AB032573; BAA92888.1; --
EMBL, AB032573; BAA92888.1; --
EMBL, AB032569; BAA92888.1; --
EMBL, AB032569; BAA92888.1; JOINED.
EMBL, AB032569; BAA92888.1; JOINED.
EMBL, AB032569; BAA92888.1; JOINED.
   EMBL; AB032571; BAA92858.1; JOINED
  FALSE_NEG.
  66515 MW;
   glucosaminyl)asparagine.
   EMBL; D89289; BAA19764.1;
   Interpro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
  Conservative
   575
365
366
  HGNC:4019; FUT8.
   PROSITE; PS50002; SH3;
   330
365
366
575 AA;
  Similarity
  10
  Golgi stack;
   602589;
  59;
  VARSPLIC
MUTAGEN
MUTAGEN
SEQUENCE
   TRANSMEM
  Query Match
Best Local :
  VARSPLIC
   DOMAIN
DOMAIN
  Genew;
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Matches
   128
   215
   385
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   Ç
   CATALYTIC ACTIVITY: GDP-L-fucose + N4-(N-acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(R(1)-alpha-1,6)-beta-D-mannosyl-1,3-(R(1)-alpha-1,6)-beta-D-mannosyl-beta-N-acetyl-1,4-N-acetyl-D-glucosaminyl)asparagine = GDP + N4-(N-acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(R(1)-alpha-1,6)-beta-D-mannosyl-1,4-beta-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-
   Q9WIS2; Q921U1;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-(1,6)-fucosyltransferase (EC 2.4.1.68) (Glycoprotein 6-alpha-L-fucosyltransferase) (GDP-fucose-glycoprotein fucosyltransferase)
(GDP-L-Fuc.N-acetyl-beta-D-glucosaminide alpha1,6-fucosyltransferase)
(alpha1-6Fucr) (Fucosyltransferase 8).
  Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the addition of fucose in alpha 1-6 linkage to
the first Glork residue, next to the peptide chains in N-glycans
69 IGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYH 128
                   glucosaminyl)asparagine.
PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: Type II membrane protein. Membrane-bound form in trans cisternae of Golgi (By similarity).
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSPERASE FAMILY 23.
  174 HVREEAQKFLRGLQVNGSR-----PGTFVGVHVRRGDYVHVMPK--VW-----
  -----YRHIPPGEYVRFIGYPCSWTFYHHLRQEILQEFTLHD
   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  445 NSLRGVILDIHFLSQA-DFLVCTFSSQV------CRVAYEIMQTLHPD 485
  Hayashi H., Yoneda A., Asada M., Ikekita M., Imamura T.; "Molecular cloning of mouse alpha-1,6-fucosyltransferase and expression of its mRNA in the developing cerebrum."; DNA Seq. 11:91-96(2000).
   ---KGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCR---ENIDTSHGD
   AA.
   575
   IISSUE=Brain;
MEDLINE=20358720; PubMed=10902914;
   STANDARD;
  129 L----NDWMEEE-
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  NCBI_TaxID=10090;
   RESULT 15
FUT9_MOUSE
ID FUT9_MOUSE
  g
   δŏ
  g
   QΫ́
  g
  δý
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EMBL; AB025198; BAA76392.1; -. EMBL; BC010666; AAH10666.1; -.

InterPro; IPR001452; SH3

MGD; MGI:1858901; Fut8

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16;
  SH3.
SH3-BINDING (POTENTIAL).
IMPORTANT FOR DONOR-SUBSTRATE BINDING.
T >> S (IN REF. 2).
Q -> E (IN REF. 2).
N -> K (IN REF. 2).
N -> K (IN REF. 2).
MW; 7BE2ED3146E0C45F CRC64;
  225 HHVVYCFMIAYGTQRTLILESQNWRYATGGWE-TVFRPVSETCTDRSGLS--TGHWS--- 278
  69 IGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAP-IFRITLPVLHSATASRIPWQNY 127
  HL----NDWMEEE----YRHIPPGEYVRFTGYPCSWTFYHHLROEILOEFTLH 172
   -HVEQHFQLLARRMQVDKKRVYLATDDPTLLKEANTKYSNYEFISDNSISWSAGLHNRYT 443
   CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
  Gaps
   14 HFILEVFTVS-----TIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQLRGMWTINA 68
   331 FVKYLIRPOPWLEKEIEEATKKLGFKHPVIGVHVRRTDKVGTEAAFHPIEEYMV-----
  173 DHYREEAQKFLRGLQVNGSR-----PGTFVGVHVRRGDYVHVMPK--VW-----
                               PROSITE; PS50002; SH3; FALSE_NEG.
Transferase; Glycosyltransferase; Transmembrane; Signal-anchor;
Golgi stack; SH3 domain.
  78;
  ----KGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCR---ENIDTSHGD 260
  ENSLRGVILDIHFLSQA-DFLVCTFSSQV-----CRVAYEINQTLHPD
  (POTENTIAL).
LUMENAL, CATALYTIC (POTENTIAL)
  Indels
  Mismatches 108;
   DB 1;
3.8;
   4.9%; Score 90;
19.8%; Pred. No.
  completed: May 27, 2003, 15:07:17
ne : 13.0683 secs
  49;
  66555 MW;
  Local Similarity 19.8
wes 58; Conservative
   563
305
366
   40
388
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
   300
   31
502
299
365
40
388
418
575 AA;
  0
   Golgi stack;
DOMAIN
   CONFLICT
CONFLICT
SEQUENCE
  TRANSMEM
   CONFLICT
   Query Match
   DOMAIN
DOMAIN
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us-10-040-863-11.rspt

Page 1

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 27, 2003, 15:01:52 ; Search time 36.6774 Seconds (without alignments) 1932.533 Million cell updates/sec Run on:

US-10-040-863-11 1850 1 MLVVQMPFSFPMAHFILFVF......AAFLPEWIGIAADLSPLLKH 344 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 segs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_21:\* Database :

1: Sp\_archea:\*
2: Sp\_archea:\*
3: Sp\_lungi:\*
4: Sp\_human:\*
5: Sp\_mammal:\*
6: Sp\_mammal:\*
7: Sp\_mhc:\*
8: Sp\_capale:\*
9: Sp\_capale:\*
10: Sp\_plage:\*
11: Sp\_rodent:\*
11: Sp\_virus:\*
13: Sp\_virus:\*
13: Sp\_virus:\*
14: Sp\_unclassified:\*
15: Sp\_runclassified:\* 

sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | O O O O                       | Description | Q9tud3 gorilla gor |        |        |        | 09ttc7 hvlobates 1 | 099450 homo sanien | 077487 bondo bydma | 077712 cercopithes | O14338 homo sapien | 029505 orvetolagis | 035087 rattus norv |        |        | Ogik44 rattus norv |        |        |
|-----------|-------------------------------|-------------|--------------------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------|--------|
| SUMMAKLES | TD.                           | 4           | Q9TUD3             | 077486 | 077485 | Q9TUD5 | Q9TTC7             | 099450             | 077487             | 077712             | 014338             | 029505             | 035087             | Q9R275 | 09JL27 | 09JK44             | 070504 | Q9TSL5 |
|           | g                             | ; i         | 9                  | 9      | 9      | 9      | 9                  | 4                  | 9                  | 9                  | 4                  | ω                  | 11                 | 11     | 11     | H                  | 11     | 9      |
|           | %<br>Duery<br>Match Length DR | 55.00       | 343                | 343    | 343    | 338    | 343                | 332                | 343                | 343                | 346                | 347                | 354                | 354    | 347    | 380                | 347    | 273    |
|           | %<br>Query<br>Match           |             | 98.7               | 98.2   | 98.1   | 6.96   | 96.5               | 95.8               | 95.5               | 93.9               | 84.7               | 82.2               | 80.2               | 80.1   | 79.8   | 79.7               | 79.5   | 76.2   |
|           | Scone                         | )           | 1825.5             | 1821.5 | 1815.5 | 1793.5 | 1784.5             | 1771.5             | 1766.5             | 1736.5             | 1566.5             | 1521.5             | 1483               | 1481   | 1475.5 | 1475               | 1471.5 | 1409.5 |
|           | Result<br>No.                 | 1           | 1                  | 2      | т      | 4      | ហ                  | ю                  | 7                  | 89                 | 6                  | 10                 | 11                 | 12     | 13     | 14                 | 15     | 16     |

| 10 0 0 0                                       | calli<br>macac<br>macac                                                                      | O91v73 mus musculu Q92v73 mus musculu Q92v72 mus spicile Q9Tty3 bos taurus Q9tty3 tos taurus Q9tubef raftus norv | Q9tty7 bos taurus<br>Q91128 mus musculu<br>P97327 mus musculu<br>Q9tud4 gorilla gor<br>Q920w5 mus musculu | 0920w4 mus spicile<br>QQtue7 hylobates 1<br>QBwxb6 homo sapien<br>QQtue6 eulemur ful<br>O14505 homo sapien | pan t<br>homo<br>homo<br>macac                 |
|------------------------------------------------|----------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|------------------------------------------------|
| 055025<br>091VF0<br>0920W2<br>0920W3<br>09TTC9 | Q9TTD0<br>Q9TUD1<br>Q9N266<br>Q920T3                                                         | 092014<br>091073<br>092012<br>0971173<br>0981186                                                                 | Q9TTY7<br>Q9JL28<br>P97327<br>Q9TUD4<br>Q920W5                                                            | Q920W4<br>Q9TUE7<br>Q8WXB6<br>Q9TUE6<br>O14505                                                             | 091UD6<br>014506<br>014507<br>091UD2<br>09N270 |
| 111111111111111111111111111111111111111        | ₩.                                                                                           | 4 <b>44</b> -                                                                                                    | 111                                                                                                       | _                                                                                                          | 04400                                          |
| 353<br>321<br>321<br>273                       | 23<br>33<br>34<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30 | 0 00 00 00 00 00 00 00 00 00 00 00 00 0                                                                          | 377<br>377<br>377<br>377                                                                                  | 377<br>365<br>365<br>365                                                                                   | 365<br>365<br>365<br>356                       |
| 44464                                          | 44000                                                                                        | 20000                                                                                                            | N N N N N N N N N N N N N N N N N N N                                                                     | നാനാനാന                                                                                                    | 0.72<br>0.72<br>0.72<br>0.72<br>0.72           |
| · · · ·                                        | 1335.5<br>1332.5<br>1311.5<br>1304.5                                                         | 1298.5<br>1298.5<br>1293.5<br>1233.5                                                                             | <ul> <li>നനനയയാ</li> </ul>                                                                                | 00<br>00.00<br>07.00                                                                                       | 1072<br>1071.5<br>1071.5<br>1071               |
| 17<br>18<br>19<br>20<br>21                     | 77<br>77<br>72<br>72<br>73<br>73                                                             | 777<br>778<br>708<br>708                                                                                         | 12 8 8 8 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                  | 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9                                                                    |                                                |
|                                                |                                                                                              |                                                                                                                  |                                                                                                           |                                                                                                            |                                                |

## ALIGNMENTS

| RESULT 1 Q9TUD3 ID Q9TUD3 D0 Q9TUD3 D1 Q9TUD3 D1 Q1-MAY-2000 (TrEMBLrel. 13, Created) D1 Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update) D1 Ol-MAY-2000 (TrEMBLrel. 10, Last annotation update) D2 D1 D1 D2 D3 D3 D3 D3 D3 D3 D3 D4 D4 D5 D5 D5 D5 D5 D5 D5 D5 D5 D5 D5 D5 D5 | FUT2. Gorilla gori Eukaryota; M<br>Mammalia; Eu<br>NCBI_TaxID=9 | AT ATLIGENE.;  TA MOL. Biol. Evol. 17:337-351(2000).  DR EMBL; AF080606; AAF14068.1;  DR InterPro; IPR002216; GT_11.  DR Pfam; PF01531; Glyco_transf_11; 1.  WY Transferase.  SO SEQUENCE 343 AA: 39001 MW; A753375D47AE8C8C CRC64; | Query Ma<br>Best Loc<br>Matches | 1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL<br> | QY 6. RGMWTINAIGREGNOMORYATLYALAKKNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120 |
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Q9TUD5;
01-MAY-2000 (TrEMBLrel. 13, Created)
   PRELIMINARY;
  Eukaryota; Metazoa;
Mammalia; Eutheria;
   Best Local Similarity
   SEQUENCE FROM N.A.
   NCBI_TaxID=9598;
  Q9TUD5
   077485;
  077485
   61
  181
  RESULT 4
   Q9TUD5
  RESULT
   077485
   AC AC
  Dp
   δy
  g
   ŏγ
  g
  g
  Óγ
  αd
  δy
   δλ
  q
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  q
   1;
  SEQUENCE FROM N.A.

Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.;

Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.;

"The old origin of a null allele se428 of the human ABO-secretor type alpha(1,2) fucosyltransferase gene (FUT2).";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
  181 KFLRGLQVNGSRPGTFVGVHVRRGDXVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF 240
   VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT 300
   121 RIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ 180
   180 KFLRGLQVNGSQPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSPIF 239
   61 RGMWTINAIGRLGNOMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120
  MEDLINE-95181460; PubMed-7876215; Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.; Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.; Sequence and expression of a candidate for the human secretor blood Jr Biol. Obem. 270:4640-4649(1995) Biol. Obem. 270:4640-4649(1995) BMS1128.11.

EMBL. ABUIGSS: BAA31128.11.

Pfam; PF01531; Glyco_transf_11; 1.
  300
   1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL 60
  1 MLVVQMPPSFPMAHFILEVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL 60
   Gaps
                          RIPWONYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ 180
RGMWTINAIGRLGNOMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120
  181 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF
   241 VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT
   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Gorilla.
   98.5%; Score 1821.5; DB 6; Length 343; 99.1%; Pred. No. 1.6e-161; Live 1; Mismatches 1; Indels 1;
   Glycosyltransferase, Transferase.
SEQUENCE 343 AA, 38973 MW; 894E28BD74AEBFBC CRC64;
  GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
  343 AA
  PRT;
   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9593;
  Alpha(1,2) fucosyltransferase.
FUT2.
  Gorilla gorilla (gorilla).
  Conservative
  PRELIMINARY;
  Similarity
  SEQUENCE FROM N.A.
  341;
   Query Match
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RA Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;
RA Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;
RA Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;
RT "Sequence and expression of a candidate for the human secretor blood
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DR EMBL, AB015634; BA31127.1;
DR Pfam; PF01531; Glyco_Lransferase.

KW Glycosyltransferase; Transferase.

"Annewed RT "Sequence As RT "Sequence
  121 RIPWONYHLNDWMEBEXRHI-PGEYVRFTGYPCSWFFYHHLRQEILQEFTLHDHVREBAQ 179
  KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF 240
   241 VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT 300
  121 RIPWQNYHUNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHURQEILQEFTLHDHVREEAQ 180
  True of origin of a null allele se428 of the human ABO-secretor type alpha(1,2) fucosyltransferase gene (FUT2).";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
  Gaps
   9
  240 VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT 299
  240 VVTSNGMAMCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT
  1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL
   RGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS
   Euteleostomi;
  1;
  Indels
   Catarrhini; Hominidae; Pan
  301 GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  300 GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLKH 343
   301 GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  Craniata; Vertebrata;
   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
   300 GGDTIYLANYTLPDSSFLKIFKPEAAFLPEWMGIAADLSPLLKH
   2;
   Score 1815.5; DB 6.
Pred. No. 5.8e-161;
1; Mismatches 2;
   AA.
   343 AA
   338
   PRT;
   Chordata;
Primates;
   98.1%;
98.8%;
  Pan troglodytes (Chimpanzee).
  Alpha(1,2)fucosyltransferase
  Matches 340; Conservative
  PRELIMINARY;
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between an intronic Alu-Y element and red cell expression of
  7 (TrEMBLrel. 03, Crea
7 (TrEMBLrel. 03, Last
2 (TrEMBLrel. 20, Last
9 fucosyltransferase.
   99.48;
   Matches 331; Conservative
   Best Local Similarity 97.4 Matches 335; Conservative
  PRELIMINARY;
   Similarity
   Similarity
  NCBI_TaxID=9606;
  01-MAY-1997
01-MAR-2002
Alpha (1,2)
   01-MAY-1997
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   Query Match
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  LQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSN 245
  246 GMANCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMIIGTFGIWAAYLTGGDTI 305
   240 GMAWCRENIDTSHGDVVFAGDGIBGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTI 299
  INAIGRIGNOMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQ 125
   NYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRG 185
   Gaps
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  90
   Biancher A.;
"Evolution of alpha2-Fucosyltransferase genes in primates: relation
  "Evolution of alpha2-Fucosyltransferase genes in primates: relation between an intronic Alu-Y element and red cell expression of ABH
  6 MPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQLRGMWT
  Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hylobatidae; Hylobates.
  Euteleostomi;
   <u>ب</u>
   96.9%; Score 1793.5; DB 6; Length 338; 98.8%; Pred. No. 6.4e-159; Live 1; Mismatches 2; Indels 1;
  요.
   Apoil P.-A., Roubinet F., Despiau S., Mollicone R., Oriol
  MEDLINE-20188794; PubMed-10723735;
Apoil P.-A., Roubinet F., Despiau S., Mollicone R., Oriol
Blancher A.;
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
NCBL_TaxID=9598;
  338 AA; 38428 MW; E7FABA0FF1BC95F9 CRC64;
   ©9TIC7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Alpha(1,2)fucosyltransferase.
         01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
  306 YLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  343 AA.
   PRT;
   MEDLINE=20188794; PubMed=10723735;
  Mol. Biol. Evol. 17:337-351(2000).
EMBL, AFR080604; ASRT4066-1; -.
InterPro. IPR002516; GT_11.
Pfam: PF01531; Glyco_transf_11; 1.
                                 Alpha (1,2) fucosyl transferase. FUT2.
  Hylobates lar (Common gibbon).
   Pan troglodytes (Chimpanzee)
   Best Local Similarity 98.8
Matches 335; Conservative
   PRELIMINARY;
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A. STRAIN=CH16;
  NCBI_TaxID=9580;
  STRAIN=TIGA;
  Transferase.
   antigens.";
   SEQUENCE
  Query Match
   Q9TIC7
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RGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120
  180
   Gaps
   "Molecular Genetic Analysis of Human Histo-blood Group System. II. Secretor Gene Inactivation by a Novel Single Missense Mutation A385T in Japanese Nonsecretor Individuals."; J. Biol. Chem. 271:8830-9837(1996).
   12 MAHFILEVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALĞPSQLRGMWTINAIGR 71
   SEQUENCE FROM N.A.
MEDLINE-96199252; PubMed=8621666;
Kudo T., Iwasaki H., Shinya N., Nishihara S., Ando T., Narimatsu I.,
Narimatsu H.;
  Gaps
  9
   9
   1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL
   181 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF
   180 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSPIF
   240 VVTSNGMANCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT
  RIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ
  241 VVTSNGMAWCRENIDISHGDVVFAGDGIEGSPAKDFALLTQCNHIIMTIGTFGIWAAYLT
   Homo sapiens (Human).
Bukaryota, Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
   DB 4; Length 332;
  Ξ,
   96.5%; Score 1784.5; DB 6; Length 343; 97.4%; Pred. No. 4.5e-158; ive 2; Mismatches 6; Indels 1;
   InterPro; IPR002516; GT_11.
Pfam; PF01531; G1yoo2transf_11; 1.
G1ycosyltransferase: Transferase:
SEQUENCE 332 AA; 37773 MW; 092A4C317DA45986 CRC64;
antigens.";
Mol. Biol. Evol. 17:337-351(2000).

EMBL; AF136648: AAR25585.1;
Interpro; IPR002516; GT_11.

Glycosyltransferase; Transferase.

SEQUENCE 343 AA; 39059 MW; A52161BE67EIF64D CRC54;
   300 GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLKH 343
  GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  Last sequence update)
Last annotation update)
  1;
   95.8%; Score 1771.5; DB
99.4%; Pred. No. 7e-157;
live 0; Mismatches
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SEQUENCE Query Match 077712 301 121 300 301 σ œ RESULT 077712 RESULT DP δλ Db g g g QΛ q δŽ an δŏ δ δ δ  $^{\circ}$ --Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.;
"The old oxigin of a null allale seds8 of the human ABO-secretor type
alpina(1,2) fucosyltransferase gene (FVT2).";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. 120 180 191 251 311 299 LGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLND 131 9 9 blood 1; Gaps RIPWQNYHLNDWMEEKYRHI-PGEYVRLTGYPCSWTFYHHLRHEILQEFTLHDHVREEAQ KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF 192 RPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSL1FVVTSNGMAWCR ENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYT MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL RGMWTINAIGRLGNOMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS RIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ WMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRGLQVNGS Pongo pygmaeus (Orangutan). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo. MEDLINE-95181460; PubMed-7876235;
MEDLINE-95181460; PubMed-7876235;
Melly R.J., Rouguler S., Glorgl D., Lennon G.G., Lowe J.B.;
"Sequence and expression of a candidate for the human secretor group alpha(1,2) fucosyltansferase gene (FUT2).";
J. Biol. Chem. 270:4640-4649(1995).
EMEL, AB015636; BAA31129.1;
InterPro; IPR002516; GT\_11.
Figur, PF01531; Glyco\_transf\_11; 1.
Glycosyltransferase: Transferase.
SEQUENCE 343 AA; 38973 MW; ZBD4DZA9704E4A0C CRC64; DB 6; Length 343; Indels 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-NOV-1998 (TrEMBLrel. 20, Last annotation update) Alpha(1,2) fucosyltransferase. Query Match 95.5%; Score 1766.5; DB 6; Best Local Similarity 95.6%; Pred. No. 2.1e-156; Matches 329; Conservative 6; Mismatches 8; 343 AA 300 LPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 332 LPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344 PRT; PRELIMINARY; SEQUENCE FROM N.A. [2] SEQUENCE FROM N.A. NCBI\_TaxID=9600; 077487 077487; 240 1 180 312 61 61 121 121 181 252 19 132 RESULT 7 077487 QQ ŏ qq  $\delta$ g qq ô QQ οy qq ŏλ δλ g  $\Omega Y$ g  $Q\underline{y}$ 

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SEQUENCE FROM N.A.
MEDLINE-99181460; PubMed=7876235;
KRELINE-99181460; PubMed=7876235;
KRELINE-99181460; Giorgi D., Lennon G.G., Lowe J.B.;
"Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fuccosyltansferase gene (FUT2).";
BIOL. Chem. 270:4640-4649(1995).

EMBL; D87934; BAA31692.1;
  Gaps
  09
   90
  Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.; Ancient origin of the null allele se428 of the human AbO-secretor locus (FUT2)."; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                241 VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT
  240 VVTSNGMAWCRENIDTSHGDVVFAGDGIGSPAKDFALLTQCNHTIWTIGTFGIWAAXLA
241 VVISNGMAWCRENIDISHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT
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   RIPWONYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ
   181 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF
   180 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDMFRAKYSSPIF
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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  Indels
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  01-NOV-1998 (TIEMBLrel. 08, Created)
01-NOV-1998 (TIEMBLrel. 08, Last sequence update)
01-NAX-2002 (TIEMBLrel. 20, Last annotation update)
Alpha(L.2)fucosyltransferase.
  9
  GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH
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nilarity 94.5%; Pred. No. 1.3e-153;
Conservative 7; Mismatches 11;
  PRT;
   InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
  Cercopithecinae; Cercopithecus.
NCBI_TaxID=37765;
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  PRELIMINARY;
   343 AA;
   Best Local Similarity
Matches 325; Conserv
   SEQUENCE FROM N.A.
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3
   248
   246
  247 MAWCRENIDISHGDVVFAGDGIEGSPAKDFALLIQCNHIIMTIGTFGIWAAYLTGGDTIY 306
  249 MAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIY 308
   NAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQN 126
   127 YHLNDWMEEEYRHIPPGEYVRFIGYPCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRGL 186
   gene
   MEDILARE FORM N.A.

Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;

Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;

"Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucosyltansferase gene (FUT2).";

J. Biol. Chem. 270:4640-4649(1995).

EMBL; D82933; BAA11638.1;

InterPro; IFR002516; GT_11.

Pfam., PF01531; Glyco_transf_11; 1.

Glycosyltransferase; Transf_11; 1.

Glycosyltransferase; Transferase.

SEQUENCE 346 AA; 39395 MW; 9D72275F8571410B CRC64;
   69
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   9 SFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL--RGMWTI 66
  01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last an office of the content of the
  QVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNG
   Koda Y., Soejima M., Liu Y., Kimura H.; "Molecular basis for secretor type alpha(1.2)-fucosyltransferase deficiency in a Japanese population: a fusion gene generated by unequal crossover responsible for the enzyme deficiency."; Am. J. Hum. Genet. 59:343-350(1996).
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  DB 4; Length 346;
  Indels
  Kimura H.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
   Last sequence update)
Last annotation update)
  23;
  Query Match

Best Local Similarity 87.3%; Pred. No. 9.7e-138;
Matches 295; Conservative 9; Mismatches 23;
   LANYILPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  347 AA
                                      346
   Created)
                                      PRT;
  SEQUENCE OF 84-106 FROM N.A.
MEDLINE=96335703; PubMed=8755920;
   01-NOV-1996 (TrEMBLrel. 01, Creat
01-JAN-1998 (TrEMBLrel. 05, Last
01-JAN-2002 (TrEMBLrel. 20, Last
Alpha (1, 2) fucosyltransferase.
HOMO Sapiens (Human).
  PARTIAL SEQUENCE FROM N.A.
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  PRELIMINARY;
  SEQUENCE FROM N.A.
   NCBI_TaxID=9606;
  029505;
   029505
  Q14338
Q14338;
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  RESULT 10
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--- FUNCTION: CREATES A MEMBERANE ASSOCIATED PRECURSOR OLIGOSACCHARIDE FUC-ALPHA((1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN ESSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE MEMBERANE-ASSOCIATED A AND B ANTIGEN SYNTHESIS PATHWAY. H AND SE ENZYMES FUCOSYLATE THE SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.
--- CATALYTIC ACTIVITY: GDP-L-FUCOSE + BETA-D-GALACTOSYL-R = GDP + ALPHA-L-FUCOSYL-1, 2-BETA-D-GALACTOSYL-R.
--- SUBCELLOLAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
   SLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWA 296
   CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
   9
   group ALPHA-2-fucosyltransferase) (GDP-L-fucose:beta-D-galactoside 2-ALPHA-L-fucosyltransferase) (ALPHA(1,2)FT) (Fucosyltransferase 3 Oryctolagus cuniculus (Rabbit).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
  1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWB--LPVQIPVLA--STSKALG
  57 PSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHS
   117 ATASRIPWONYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFILHDHVR
  177 EEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYS
  -i- TISSUE SPECIFICITY: ADULT GASTROINTESTINAL TRACT AND COLON.
-i- MISCELLANEOGOS: THERE ARE IHREE CENES (FUTI, FUT2 AND FUT3) WHI
ENCODE GALACTOSIDE 2-1-FUCOSYLTRANSFERASE IN RABBIT. THEY ARE
EXPRESSED IN A TISSUE-SPECIFIC MANNER.
-i- SIMILARITY: STRUCTURAL SIMILARITY WITH THE OTHER MAMMALIAN
GIXCOSYLTRANSFERASE SIMILARITY WITH THE OTHER MAMMALIAN
EMBL; X91269; CAA62669.1; -.
  rabbit GDP-L-
  LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. ) (POIENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

746F7007309862A5 CRC64;
  82.2%; Score 1521.5; DB 6; Length 347; 81.6%; Pred. No. 1.5e-133;
  InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack.
  AYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  SEQUENCE FROM N.A.

TISSUB-GASTROINTESTINAL TRACT;

MEDLINE-96279281; PubMed-8663168;

Hitoshi S., Kojinna N., Kanazawa I., Tsuji S.;

"Molecular cloning and expression of a third type of ral fucose.beta D-galactosiae.2 alpha-L-fucosyitransferase.'

J. Biol. Chem. 271:16575-16981(1996).

-i- FUNCTION: CREATES A MEMBRANE-ASSOCIATED PRECURSOR OI
  Mammaiia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
  40;
  19; Mismatches
  347 LU
192
286
312 N-
39469 MW;
  Matches 284; Conservative
   29
192
186
286
312
347 AA;
   Query Match
Best Local Similarity
   Ø
  NCBI_TaxID=9986;
  Signal-anchor;
DOMAIN
   CARBOHYD
  CARBOHYD
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  CARBOHYD
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   DOMAIN
  180
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1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQ- 59
  Matches 276;
  09JL27
  230
   121
  RESULT 13
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  3;
  289
   169
   299
   170 TLHDHVREEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALD 229
   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
  Gaps
   1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAM--WELPV------QIPVLA 49
   9
  Bureau V., Marionneau S., Cailleau-Thomas A., Le Moullac-Vaidye B.,
  180 ILHDHVREEAQAFIRGIRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALD
   50 SISKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI
  110 TLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGGFYVRFTGYPCSWTFYHHLRQEILQEF
  230 WFRARYSSLIFYVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTI
  240 MFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLIQCNHTIMTI
  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
  GTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
   12;
  80.2%; Score 1483; DB 11; Length 354; 77.7%; Pred. No. 6.1e-130; Live 30; Mismatches 37; Indels 12
  fucosyltransferase genes.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB006138; BA21742.1;
InterPro; IPR002516; GI_11:
Pfam; PF01331; Glyco_transf_11; 1.
Glycosyltransferase: Transferase.
EQUENCE 354 AA, 39995 MW; 8636444888215BA1 CRC64;
   Soejima M., Wang B., Koda Y., Kimura H.; "Two distinct rat GDP-L-fucose:b-D-galactoside 2-a-L-
  Last annotation update)
   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
  Last sequence update)
   354 AA
   354
  01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last seq
01-WAR-2002 (TrEMBLrel. 20, Last ann
  PRT;
  MEDLINE=21099374; PubMed=11179967;
   PRT;
  Alpha 1,2-fucosyltransferase.
FTB.
Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata,
Mammalia; Eutheria; Rodentia;
   Alpha 1,2-fucosyltransferase
FTB.
  Matches 276; Conservative
   PRELIMINARY;
   Rattus norvegicus (Rat)
   PRELIMINARY;
  SEQUENCE FROM N.A.
TISSUE=COLON CANCER;
   Similarity
  SEQUENCE FROM N.A.
   NCBI_TaxID=10116;
  NCBI_TaxID=10116
   STRAIN=BDIX
   Query Match
Best Local S
   09R275
   035087
   300
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   RESULT 12
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169
  50 STSKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI 109
  Gaps
  Gaps
  1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAM--WELPV------QIPVLA 49
  Domino S.E., Zhang L., Lowe J.B.;
"Molecular Cloning, Genomic Mapping, and Expression of Two Secretor Blood Group alpha (1,2)Fuccosyltransferase Genes Differentially Trequiated in Mouse Uterine Epithelium and Gastrointestinal Tract.", J. Blol. Chem. 276:23748-23756(2001).

EMBL. AF21465; AR45146:1; BMGD; MGD; MGD; MCD; FLL2.
InterPro; IPR002516; GT_11
   SLPVLHSDTAKKIPWQNY=LNDWAEERYRHI-PQHFVRFTGYPCSWTFYHHLRPEILKEF
   240 MFRARYSSPYFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTI
   170 TLHDHVREEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALD
   WFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIBGSPAKDFALLTQCNHTIMTI
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
  110 TLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEF
  GTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
   DB 11; Length 347;
  12;
Liehr T., Le Pendu J.;
"Comparison of the three rat GDP-L-fucose: beta-D-galactoside alpha-L-fucosyltransfarases FTA, FTB and FTC.";
Eur. J. Biochem. 268:1006-1019(2001).
EMBL; AF131238; AAD24469.1;
InterPro: IPR002516; GT.11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferaes; Transf_erase.
SEQUENCE 354 AA, 39983 MW; 123EBC8379EB559E CRC64;
  Length 354;
  300 GTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKH
   38; Indels
   Indels
  DD5F441046CC8E79 CRC64;
   01-OCT-2000 (TrEMBLrel. 15, Created)
1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha(1,2)fucosyltransferase FUT2 (EC 2.4.1.69).
PUT2.
  Score 1481; DB 11;
Pred. No. 9.4e-130;
   79.8%; Score 1475.5; DB 79.3%; Pred. No. 3e-129;
  347 AA
   29; Mismatches
  30; Mismatches
  Pfam; PF01531; Glyco_transf 11; 1.
Glycosyltransferase; Transferase.
SEQUENCE 347 AA; 39243 MW; DD5E
  PRT;
   STRAIN=129/OLA;
MEDLINE=21316545; PubMed=11323419;
  80.1%;
77.7%;
  Query Match 79.8'
Best Local Similarity 79.3'
Matches 276; Conservative
   Conservative
  PRELIMINARY;
   Mus musculus (Mouse)
   Query Match
Best Local Similarity
   SEQUENCE FROM N.A.
  NCBI_TaxID=10090;
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01-AUG-1998
  2.4.1.69).
   Query Match
  070504
   117
   180
   RESULT 15
070504
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   QΥ
  δŏ
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   3;
   Sherwood A.L., Stroud M.R., Levery S.B., Holmes E.H.;

"An amino acid region at the N-terminus of rat hepatoma H35 cell GDP-fucose:GM1 alpha 1-2 fucosyltransferase is required for optimum enzyme activity and interaction with lipids.";

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF264005; AAF72200.1;

InterPro: IPR00216; GT_11.

Pfam; PF01531; Glyco_transf_11; 1.

Glycosyltransferase; Transferase.

SEQUENCE 380 AA; 42742 MW; 920692C96689C05C CRC64;
  169
  SLPVLHSDTAKKIPWQNYHLNDWMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEF 179
  240 MFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHIIMTI 299
   180 TLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALD 239
   50 STSKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI 109
  EEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYS 236
  Gaps
   SLIFVVTSNGMAWCRENIDISHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWA 296
   Alpha 1-2 fucosyltransferase.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
   1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAM--WELPV------QIPVLA 49
  170 TLHDHVREEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALD
  110 TLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEF
  WFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTI
ATASRIPWQNYHINDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVR
                                      60 ---LRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHS
   12;
  79.7%; Score 1475; DB 11; Length 380; 77.7%; Pred. No. 3.8e-129; Live 30; Mismatches 37; Indels 12
   297 AYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  300 AYLAGGDTIYLANYTLPDSPFLKIFKPAAAFLPEWMGIPADLSPLLKH
  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
   380 AA
   PRT;
   275; Conservative
   PRELIMINARY;
  Similarity
   SEQUENCE FROM N.A.
  NCBI_TaxID=10116;
  STRAIN-FISCHER;
   Query Match
Best Local 9
   Q9JK44
  121
   Matches
   117
   180
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  Q9JK44
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EBAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYS 236
  240 SPVEVVTSNGMAWCRENINTSLGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWA 299
   SLIFVVTSNGMANCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWA 296
   Gaps
   "GDP-fucose: beta-galactoside alphal,2-fucosyltransferase, MFUT-II, and not MFUT-I or -III, is induced in a restricted region of the digestive tract of germ-free mice by host-microbe interactions and cycloheximide.";
  60 ---LRGMWIINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMBSTLAPIFRITJPVLHS
  1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWBLPVQIPVLASTSKALGPSQ-
   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
  Length 347;
   5
   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
GTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLK
                      300 GTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
  SEQUENCE FROM N.A.
STRAIN=ICR: TISSUE-CASTROINTESTINAL TRACT;
MEDILINE-20471982; Pubmed=11018479;
Lin B. Hayashi Y., Saito M., Sakakibara Y., Yanagisawa M.,
Iwamori M.;
  297 AYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
  InterPro; IPR002516; GT_11.
Pfan; PF01531; G1yoc_transf_11; 1.
G1ycosylltransferase; Transferase.
SEQUENCE 347 AA; 39215 MM; 616CCB11581C4179 CRC64;
  11;
  DB
   79.5%; Score 1471.5; DB
   AA
  pred. No. 7e-.
30; Mismatches
   cycloheximide.";
Biochim. Biophys. Acta 1487:275-285(2000).
EMBL; AF064792; AAC16887.1; -.
   Created)
   Search completed: May 27, 2003, 15:10:47 Job time: 37.6774 secs
   Conservative
  (TrEMBLrel.
   PRELIMINARY;
   MGD; MGI:109374; Fut2.
   Best Local Similarity
Matches 275; Conserv
  NCBI_TaxID=10090;
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